

OM nucleic - nucleic search, using sw model

Run on: April 3, 2004, 00:09:01 ; Search time 3852.78 Seconds
(without alignments)
16863.481 Million cell updates/sec

Title: US-10-030-269A-1
Perfect score: 1499
Sequence: 1 gcggctgcagcggctgtta.....taaatgtttttattctctc 1499

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_on:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_cm:*
- 21: em_or:*
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- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htg_mus:*

- 34: em_htg_pln:*
- 35: em_htg_rod:*
- 36: em_htg_mam:*
- 37: em_htg_vrt:*
- 38: em_sy:*
- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB | ID | Description |
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| 1 | 1499 | 100.0 | 1499 | 6 | AX136089 | AX136089 Sequence |
| 2 | 1499 | 100.0 | 1499 | 6 | BD093294 | BD093294 Amyloid b |
| 3 | 1499 | 100.0 | 1499 | 6 | BD123497 | BD123497 Secretary |
| 4 | 1499 | 100.0 | 1499 | 9 | AK075335 | AK075335 Homo sapi |
| 5 | 1494.2 | 99.7 | 1504 | 6 | BD063628 | BD063628 Human pro |
| 6 | 1483.8 | 99.0 | 1519 | 6 | BD186179 | BD186179 STAT6 act |
| 7 | 1481.6 | 98.8 | 1533 | 9 | BC001106 | BC001106 Homo sapi |
| 8 | 1450 | 98.7 | 1562 | 6 | BD170687 | BD170687 NF-kappa |
| 9 | 1478 | 98.6 | 1503 | 6 | BD186178 | BD186178 STAT6 act |
| 10 | 1475 | 98.4 | 1552 | 6 | AX086058 | AX086058 Sequence |
| 11 | 1475 | 98.4 | 1552 | 9 | HSMB01574 | AX136600 Homo sapi |
| 12 | 1474.4 | 98.4 | 1552 | 9 | AK091726 | AK091726 Homo sapi |
| 13 | 1473.6 | 98.3 | 1564 | 6 | AX376178 | AX376178 Sequence |
| 14 | 1473.6 | 98.3 | 1564 | 6 | AX696999 | AX696999 Sequence |
| 15 | 1473.6 | 98.3 | 1564 | 9 | AY359012 | AY359012 Homo sapi |
| 16 | 1472 | 98.2 | 1544 | 9 | AK054883 | AK054883 Homo sapi |
| 17 | 1469.6 | 98.0 | 1571 | 6 | AR400559 | AR400559 Sequence |
| 18 | 1469.6 | 98.0 | 1571 | 6 | AX013063 | AX013063 Sequence |
| 19 | 1469.6 | 98.0 | 1571 | 6 | BD206244 | BD206244 Human nuc |
| 20 | 1175.4 | 78.4 | 2892 | 6 | AX833111 | AX833111 Sequence |
| 21 | 1175.4 | 78.4 | 2892 | 9 | AK094588 | AK094588 Homo sapi |
| 22 | 1043.4 | 69.6 | 132131 | 9 | AX139159 | AX139159 Human DNA |
| 23 | 761 | 50.8 | 1791 | 6 | AY138587 | AY138587 Homo sapi |
| 24 | 605.8 | 40.4 | 610 | 9 | AY138587 | AY138587 Homo sapi |
| 25 | 583.8 | 38.9 | 1445 | 10 | BC016524 | BC016524 Mus muscu |
| 26 | 557.6 | 37.2 | 1134 | 6 | AR341541 | AR341541 Sequence |
| 27 | 557.6 | 37.2 | 1134 | 6 | BD209735 | BD209735 Compositi |
| 28 | 548.8 | 36.6 | 552 | 9 | AB013909 | AB013909 Homo sapi |
| 29 | 545.8 | 36.4 | 549 | 6 | BD063603 | BD063603 Human pro |
| 30 | 544.4 | 36.3 | 575 | 6 | AX136453 | AX136453 Sequence |
| 31 | 544.4 | 36.3 | 575 | 6 | BD123693 | BD123693 Secretary |
| 32 | 422.4 | 28.2 | 446 | 6 | AR424082 | AR424082 Sequence |
| 33 | 422.4 | 28.2 | 446 | 6 | BD119635 | BD119635 EST and e |
| 34 | 397.4 | 26.5 | 542 | 6 | AR412544 | AR412544 Sequence |
| 35 | 397.4 | 26.5 | 542 | 6 | BD108097 | BD108097 EST and e |
| 36 | 380.4 | 25.4 | 404 | 6 | AR413779 | AR413779 Sequence |
| 37 | 380.4 | 25.4 | 404 | 6 | BD109332 | BD109332 EST and e |
| 38 | 348.8 | 23.3 | 407 | 6 | AX884371 | AX884371 Sequence |
| 39 | 348.8 | 23.3 | 407 | 6 | BD023981 | BD023981 Sequence |
| 40 | 292.2 | 19.5 | 2072 | 5 | BC045338 | BC045338 Danio rer |
| 41 | 282.4 | 18.8 | 411 | 11 | G23808 | G23808 human STS W |
| 42 | 274 | 18.3 | 277 | 11 | G21487 | G21487 human STS W |
| 43 | 265.2 | 17.7 | 292 | 6 | BD060681 | BD060681 Secreted |
| 44 | 259.6 | 17.3 | 287 | 6 | AX156250 | AX156250 Sequence |
| 45 | 238.2 | 15.9 | 237879 | 2 | AC139893 | AC139893 Rattus no |

ALIGNMENTS

RESULT 1
AX136089
LOCUS
DEFINITION
AX136089
ACCESSION
AX136089.1 GI:14272497
VERSION
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Oka.T., Isogai.T., Nishikawa.T., Kawai.Y., Sugiyama.T. and
Hayashi.K.
TITLE
Secretory protein or membrane protein
JOURNAL
Patent: EP 1067182-A 11 10-JAN-2001;
Helix Research Institute (JP)
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ORIGIN

Query Match 100.0%; Score 1499; DB 6; Length 1499;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGCTGAGCGGGCTTGTAGGTGTCCGGCTTTGCTGGCCAGCAAGCTTGATAGCATG 60
Db 1 GGGGCTGAGCGGGCTTGTAGGTGTCCGGCTTTGCTGGCCAGCAAGCTTGATAGCATG 60
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Db 121 AAGAGTTCTGAAGATATCCGGTGCMAATGCATCTCTCCACTTATAGAAACATCAGTGGG 180
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Qy 541 CAGCGGTGGAGGCTGCAGGTGCAGGAGCAGCGGAGACAGTCTTCGATCGGCAAGATG 600
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[illegible]

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 QY 1081 CAGCGCTCAGGCCOCCAGCCOCCAGCTCCAGGCCCTGAGGACAGCTCTGATGGAGAGCTGGG 1140
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RESULT 3

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 DEFINITION Secretory protein or membrane protein.
 ACCESSION BD123497
 VERSION BD123497.1 GI:23218442
 KEYWORDS JP 2002017376-A/6.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
 SECRETORY PROTEIN OR MEMBRANE PROTEIN
 PATENT: JP 2002017376-A 6 22-JAN-2002;
 HELIX RESEARCH INSTITUTE
 OS Homo sapiens (human)
 PN JP 2002017376-A/6
 PD 22-JAN-2002
 PF 07-JUL-2000 JP 2000253173
 PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,YURI KAWAI,TOMOYASU
 PI SUGIYAMA,
 PI KOJI HAYASHI
 PC
 C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC

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 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 1 GCGGCTGCAGCGGGCTTGTAGGTGTCCGGCTTTGCTGGCCCGCCAGCTGAGGCCAAC 60
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Ekaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 Ota,T., Nishikawa,T., Suzuki,Y., Kawai-Hio,Y., Hayashi,K., Ishii,S., Saito,K., Yamamoto,J., Wakamatsu,A., Nagai,T., Nakamura,Y., Nagahara,K., Sugano,S. and Isogai,T., HRI human cDNA sequencing project Unpublished 2 (bases 1 to 1499) Isogai,T. and Yamamoto,J. Direct Submission Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass sequencing, clone selection and full insert sequencing; Helix Research Institute (supported by Japan Key Technology Center etc.); cDNA library construction; Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center. FEATURES source 1..1499 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="NT2RM1000853" /cell_lines="NT2" /cell_type="teratocarcinoma" /clone_lib="NT2RM1" /notes="cloning vector: pUC19FL3-mRNA from uninduced NT2 neuronal precursor cells" 58..609 /notes="unnamed protein product" /codon_start=1 /protein_id="BAC11554.1" /db_xref="GI:22761357" /translation="MKLLSLVAVGCLVPPAAEANKSSEDIRCKICPEPVN1SGHIY NQNVSKDQNCILHVPEFVPGHDEYACILCEERYEERTTTIKVIIIVISVGLAL LLYMFMIVDPLIRKPDAYTOLHNEENEDARSMAAAAASLGGFRANTVLERVEGA QQRWKLVQEQRKTVFDRHKMLS" ORIGIN Query Match 100.0%; Score 1499; DB 9; Length 1499; Best Local Similarity 100.0%; Pred. No. 0; Matches 1499; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 GCGGCTGCAGCGGGCTTTGTAGGTGTCGGCTTTCGTCGCCAGCAAGCCTGATAGCATG 60 Db 1 GCGGCTGCAGCGGGCTTTGTAGGTGTCGGCTTTCGTCGCCAGCAAGCCTGATAGCATG 60 Qy 61 AAGCTCTTATCTTTGGTGGCGGTGTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 120 Db 61 AAGCTCTTATCTTTGGTGGCGGTGTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120 Qy 121 AAGAGTTCTGAAGATATCCGGTGCATATGCATCTGTCCATTAAGAACATCAGTGGG 180 Db 121 AAGAGTTCTGAAGATATCCGGTGCATATGCATCTGTCCATTAAGAACATCAGTGGG 180 Qy 151 CATATTATACACCAAGATATCCAGAGGACTGCAACTGCTGCAGTGGTGGAGCCC 240 Db 151 CATATTATACACCAAGATATATCCAGAGGACTGCAACTGCTGCAGTGGTGGAGCCC 240 Qy 241 ATGCCAGTGCCTGCCCATGAGTGGAGGCTACTGCCTGCTGTGGAGTACAGTACAG 300 Db 241 ATGCCAGTGCCTGCCCATGAGTGGAGGCTACTGCCTGCTGTGGAGTACAGTACAG 300 RESULT 4 AK075335 1499 bp mRNA linear PRI 03-SEP-2002 LOCUS Homo sapiens cDNA PSEC0012 fis, clone NT2RM1000853. DEFINITION AK075335 ACCESSION AK075335.1 GI:22761356 VERSION oligo capping; fis (full insert sequence). KEYWORDS Homo sapiens (human) SOURCE ORGANISM Homo sapiens

| | | | | | | | | | | | | | | | | | | | | | | | |
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| QY | 1261 | CAC | TTG | AGGG | GT | GGG | GAG | T | CC | TCT | CT | CC | CA | GT | GT | CC | CA | GT | CA | CTG | AG | 1320 | |
| D6 | 1261 | CAC | TT | GAG | GGG | GT | GGG | CA | T | CC | TCT | CT | CC | CA | GT | GT | CC | CA | GT | CA | CTG | AG | 1320 |
| QY | 1321 | GT | CGG | TT | GGA | CA | CAT | GAG | CT | GAG | CGT | GAG | CT | GAG | CA | CA | CA | CA | CA | CA | CA | 1380 | |
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| QY | 1381 | TGG | GGT | GC | CT | GT | GC | CT | GA | CT | CG | GT | CT | CC | CA | GT | GT | GT | GT | GT | GT | 1440 | |
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| | |
|------------|---|
| RESULT 5 | |
| B06G36Z8 | |
| LOCUS | B06G36Z8 1504 bp DNA linear PAT 27-AUG-2002 |
| DEFINITION | Human proteins having transmembrane domains and DNAs encoding these proteins. |
| ACCESSION | B06G36Z8 |
| VERSION | B06G36Z8.1 GI:22609231 |
| KEYWORDS | JP 2001508407-A/43. |
| SOURCE | Homo sapiens (human) |

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 1504)
Kato, S., Sekine, S., Kimura, T. and Kobayashi, M.
Human proteins having transmembrane domains and DNA encoding these

JOURNAL
proteins
human; proteins having transmembrane domains and low molecular
weight

| | | | |
|---------|-------------------------|-----------------------|---|
| COMMENT | OS Homo sapiens (human) | PN JP 2001508407-A/43 | SAGAMI CHEMICAL RESEARCH CENTER, FUKUOKA INC. |
|---------|-------------------------|-----------------------|---|

| | |
|----|---------------------------|
| PD | 26-JUN-2001 |
| PF | 07-NOV-1997 JP 1998522374 |
| PR | 13-NOV-1996 JP 8/301429 |

PI SEISHI KATO, SHINGO SEKINE, TOMOKO KIMURA, MIDORI KOBAYASHI PC
C12N15/12, C07K14/705, C12N5/10, C12N15/57, C12N9/48, C12N9/14, PC
C12N15/55

| | |
|--------------------------|---------------------|
| CC Strandedness: Double; | |
| CC Topology: Linear; | |
| EH Key | Location/Qualifiers |

| FT | CDS | Location/Qualifiers |
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ORIGIN

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| Best Local Similarity | 99.8% | Pred. No. 0 | | |
| Matches 1496: Conservative | 0 | Mismatches 3 | Indels 0 | Gaps 0 |

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.....

| GOIN33/15, C GOIN33/50, GOIN33/53, GOIN33/566, GOE17/30, GOE17/60 CC | STAIN6 |
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| activating gene | |
| H Key | Location/Qualifiers |
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| Best Local Similarity | 99.8%; | Pred. No. 0; | | |
| Matches 1496: Conservative | 0; | Mismatches | 2; | Indels 1; |
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[illegible]

RESULT. T 7

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LOCUS
DEFINITION
IMAGE:3506442), complete cds.
EC001106
VERSION
EC001106.2
KEYWORDS
SOURCE
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Gr:33875996
NGC.
Homo sapiens transmembrane protein 9, mRNA (cDNA clone MGC:591 linear 1533 bp mRNA PRI 04-OCT-2003

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusik, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Donald, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Frange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullen, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002); 22388257

MEDLINE 12477932

PUBLISHED 2 (bases 1 to 1533)

REFERENCE Strausberg, R.

AUTHORS Direct Submission

TITLE Submitted (11-DEC-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

JOURNAL NIH-MGC Project URL: <http://mgc.nci.nih.gov>
On Aug 19, 2003 this sequence version replaced gi:12654544.
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/BTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettman, Anuradha Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting

REMARK
COMMENT Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Series: IRAL Plate: 7 Row: b Column: 23
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24308523.
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Dd 375 CTGTTGCTCTACATGGGCTTCTGATGCTGGTGGACCTCTGATCCGAAAGCCGATGCA 434
Qy 421 TACACTGAGCAACTGCAATGAGGAGGAGATGAGGATCTCGCTCTATGGCAGCAGCT 480
Dd 435 TACACTGAGCAACTGCAATGAGGAGGAGATGAGGATCTCGCTCTATGGCAGCAGCT 494
Qy 481 GCTGCATCCCTCGGGGGACCCGAGCAACACAGCTCTCGAGCGTGTGGAGGTGCCAG 540
Dd 495 GCTGCATCCCTCGGGGGACCCGAGCAACACAGCTCTCGAGCGTGTGGAGGTGCCAG 554
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| LOCUS | BD170687 | 1562 bp | DNA linear PAT 17-JAN-2003 |

RESULT 8
BD170687
TODIS

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| Qy | 61 | AAGCTCTTATCTTTGTTGGCGGTGGTGGGTGTTTGTGTGGCCCAAGCTGAAGCCAAAC | 120 |
| Db | 123 | AAGCTCTTATCTTTGTTGGCTGTGTGGGTGTTTGTGTGTGGCCCAAGCTGAAGCCAAAC | 182 |
| Qy | 121 | AAGAGTTCTGAAGATATCCGGTGCMAATGCATCTCTCCACCTTTATGAACAATCAAGTGGG | 180 |
| Db | 183 | AAGAGTTCTGAAGATATCCGGTGCMAATGCATCTCTCCACCTTTATGAACAATCAAGTGGG | 242 |
| Qy | 181 | CATATTACCAACCGAAGTATATCCAGAGAGGACTGCACATGCTGCACGTGTTGGAGGCC | 240 |
| Db | 243 | CACATTTACCAACCGAAGTATATCCAGAGAGGACTGCACATGCTGCACGTGTTGGAGGCC | 302 |
| Qy | 241 | ATGCCAGTGCTGGCCATGAAGTGGAGGCGCTACTGCCTGTGTGGAGTGCAGGTAAGAG | 300 |
| Db | 303 | ATGCCAGTGCTGGCCATGAAGTGGAGGCGCTACTGCCTGTGTGGAGTGCAGGTAAGAG | 362 |

| | | | |
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| Qy | 1 | GGGGCTGCAGGGGGCTTGTAGGTGTCCGGCTTTGCTGGCCAGCAAGCCTGATAACATG | 60 |
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| Db | 243 | CACATTTACCAACCGAAGTATATCCAGAGAGGACTGCACATGCTGCACGTGTTGGAGGCC | 302 |
| Qy | 241 | ATGCCAGTGCCTGGCCATGAAGTGGAGGCGCTACTGCCTGTGTGGAGTGCAGGTAAGAG | 300 |
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| QY | 1320 | GCTCGTGTGGAAACATGAGCACTCGAGGCTGAGCGTGGATCTGAACACACAGCGCCCTGTAC | 1379 |
| | | | |
| DB | 1363 | GCTCGTGTGGAAACATGAGCACTCGAGGCTGAGCGTGGATCTGAACACACAGCGCCCTGTAC | 1442 |
| QY | 1380 | TTGGGTTGCCTCTCTGTTCCTGACACTTCGTCTACCACTGCATGGAGAGAAAATTTTGTCC | 1439 |
| | | | |
| DB | 1443 | TTGGGTTGCCTCTCTGTTCCTGACACTTCGTCTACCACTGCATGGAGAGAAAATTTTGTCC | 1502 |
| QY | 1440 | TCTGTGCTTAGAGTTGTGTGAATACAGGAGCGCATATTAATGTGTTTATCTCTCTC | 1499 |
| | | | |
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| | Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. | | | |

REFERENCE
AUTHORS
TITLE
JOURNAL
1 (bases 1 to 1503)
Honda,G., Matsuda,A., Muramatsu,S. and Ishizawa,K.
STAT6 activating gene
Patent: WO 02096943-A, 47 05-DEC-2002:
ASHI KASEI CORP, GOICHI HONDA, AKITO MATSUDA, SHUJI MURAMATSU, KENYA
ISHIZAWA

| OS | Hom sapiens (human) |
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| EN | WO 02096943-A/47 |
| ED | 05-DEC-2002 |
| PF | 22-MAY-2002 |
| PR | 25-MAY-2001 JP 01P 157043, 30-AUG-2001 JP 01P 260681 PR |
| PI | 10-OCT-2001 JP 01P 313175 |
| PC | GOICHI HONDA-AKIO MATSUDA, SHUJI MURAMATSU, KENYA ISHIZAWA PC COTK14/47, COTK17/00, C12N15/12, C12N5/10, C12P21/02, C12P21/06, PC C12P1/02, |

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| Db | 1026 | CCAGCAATTCAGCACTGTGTCTCTTCAGTGGTTC-TTAAACCACTCCCTCCCAAGCC | 1085 |
| Qy | 1030 | CCAGGCGCTCAGCCCAAGCCCAAGCTCCAGCGCTGAGAGACAGCTCTGATGGAGAGCTGG | 1139 |
| Db | 1086 | CCAGGCGCTCAGCCCAAGCCCAAGCTCCAGCGCTGAGAGACAGCTCTGATGGAGAGCTGG | 1145 |
| Qy | 1140 | GCCCGCTCAGCCCACTGGGTTCTCAGGCGTGCATCGAAAGCTGGTGTTCGCTGTCCCTGT | 1199 |
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| Qy | 1200 | GCACTTCTCGCACTGGGGCATTGAGTGCCCAATGCATACTCTGCTGCCGGTCCCTCACTC | 1259 |
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| Qy | 1260 | GCACTTGAAGGGTCTGGGCACTCCCTCCTCTCCCAAGTGTCCACAGTCACTGAGCCAGAC | 1319 |
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| Qy | 1320 | GGTGGTGGAAATAGACATCAGACATCGAGCGCTGAGCGTGGATCTGAAACCAACAGCCCTGTAC | 1379 |
| Db | 1326 | GGTGGTGGAAATAGACATCAGACATCGAGCGCTGAGCGTGGATCTGAAACCAACAGCCCTGTAC | 1385 |
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| Qy | 1440 | TCTGTCTTAGAGTGTGTGTAAATCAAGAGAGCCCATTAATGTGTTTATTCTC | 1497 |
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 Db 144 AAGATTTCTGAAGATATCCGGTGCATAATGCACTCTGCAACCTTATGAACAATCATGTGG 203
 QY 181 CATATTTACACAGATGATCCCGAAGGACT-----GCAACTGCTGCACTGCTG 234
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 QY 235 GAGCCATGCCAGTGGCTGGCCATGACGTGGAGGCTACTGCTGCTGCTGCTGCTGCTGCTG 294
 Db 264 GAGCCATGCCAGTGGCTGGCCATGACGTGGAGGCTACTGCTGCTGCTGCTGCTGCTGCTG 323
 QY 295 TAGGAGGAGCGAGACCAACCAATCAAGGTGATCATTTGTGATCTAGCTGCTGCTGCTGCTG 354
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RESULT 11
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 DEFINITION Homo sapiens mRNA; cDNA DKFp564I1216 (from clone DKFp564I1216);
 complete cds.
 ACCESSION AL136600
 VERSION AL136600.1 GI:13276700
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1552)
 AUTHORS Blum,H., Bauersachs,S., Newes,H.W., Gassenhuber,J. and Wiemann,S.
 TITLE Direct Submission
 JOURNAL Submitted (12-MAR-2002) MIPS, Am Klopferspitze 18a, D-82152
 Martinsried, GERMANY
 COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by LMU (Ludwig Maximilians University,
 Munich/Germany) within the cDNA sequencing consortium of the German

Genome Project.
This clone (DKFZp564I1216) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de Further
information about the clone and the sequencing project is available
at <http://mips.gsf.de/proj/cDNA/>.

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ORIGIN

Query Match 98.4%; Score 1475; DB 9; Length 1552;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1494; Conservative 0; Mismatches 5; Indels 6; Gaps 1;
QY 1 CGCGCTGACGCGGCTTTAGTGTCCGGCTTTGCTGGCCGACGAGCCTGATAGCATG 60
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DEFINITION AK091726
VERSION AK091726.1 GI:21750165
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Oshima,A., Takahashi-Fujii,A., Tanase,T., Inose,N., Takeuchi,K.,
Arita,M., Mueshino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R.,
Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,
Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,
Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,
Wagatsuma,M., Murakawa,K., Kanehori,K., Sugiyama,A., Kawakami,B.,
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Isogai,T.
TITLE NEBO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1959)
AUTHORS Isogai,T. and Yamamoto,J.
TITLE Direct Submission
JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team): 2-6-7
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEBO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
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Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.

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DEFINITION Sequence 245 from Patent WO0168848.
ACCESSION AX376178
VERSION AX376178.1 GI:19170481
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1
REFERENCE
AUTHORS Bakker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P., J.,
Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and
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 Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
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 Goddard,A., Wood,W.I. and Godowski,P.
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 A Bioinformatics Assessment
 JOURNAL Genome Res. 13 (10), 2263-2270 (2003)
 PUBMED 12975309
 REFERENCE 2 (bases 1 to 1564)
 Clark,H.F.
 TITLE Direct Submission
 JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
 Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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Db 1044 CTGGTCTTCAGGAATCAGTCTCTGGGAGGAAGCATGCCCCAGCATTCAGCATGTGT 1103
QY 1040 CCTTTCTGCAGTGGTTCCTTATCACAACCTCCCTCCAGCCCAAGGCGCTCAGGCCAGCC 1099
Db 1104 CCTTTCTGCAGTGGTTCCTTATCACAACCTCCCTCCAGCCCAAGGCGCTCAGGCCAGCC 1163
QY 1100 CCAAGTCCAGCCCTGAGGACAGCTCTGATGGAGAGCTGGGCCCCCTGAGCCACTGGGT 1159

OM nucleic - nucleic search, using sw model

Run on: April 2, 2004, 21:47:00 ; Search time 375.536 Seconds
(without alignments)
16957.243 Million cell updates/sec

Title: US-10-030-269A-1
Perfect score: 1499
Sequence: 1 gcggctgcagcggcttgta.....taaattgtttatttcttc 1499

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 3
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04.*
1: geneseqn1980s.*
2: geneseqn1990s.*
3: geneseqn2000s.*
4: geneseqn2001as.*
5: geneseqn2001bs.*
6: geneseqn2002s.*
7: geneseqn2003as.*
8: geneseqn2003bs.*
9: geneseqn2003cs.*
10: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result | Nc. | Score | Query | Match | Length | DB | ID | Description |
|--------|--------|-------|-------|-------|----------|----|----|--------------------|
| 1 | 1499 | 100.0 | 1499 | 4 | AAF29357 | | | Aaf29357 Amyloid-b |
| 2 | 1499 | 100.0 | 1499 | 5 | AAF93749 | | | Aaf93749 Human cDN |
| 3 | 1494.2 | 99.7 | 1504 | 2 | AAV49584 | | | Aav49584 Human sto |
| 4 | 1481.6 | 98.8 | 1937 | 5 | ABV23182 | | | Abv23182 Human pro |
| 5 | 1481.4 | 98.8 | 1645 | 3 | AAF21831 | | | Aaf21831 Human bre |
| 6 | 1480 | 98.7 | 1562 | 6 | ABQ91986 | | | Abq91986 Human NF- |
| 7 | 1479.6 | 98.7 | 1565 | 3 | AAA39939 | | | Aaa39939 Human TAN |
| 8 | 1475 | 98.4 | 1552 | 5 | ABX71217 | | | Abx71217 Human tra |
| 9 | 1473.6 | 98.3 | 1564 | 3 | AAA37041 | | | Aaa37041 Human PRO |
| 10 | 1473.6 | 98.3 | 1564 | 4 | AAF54249 | | | Aaf54249 DNA encod |
| 11 | 1473.6 | 98.3 | 1564 | 4 | AAS46047 | | | Aas46047 Human DNA |
| 12 | 1473.6 | 98.3 | 1564 | 7 | ABX78650 | | | Abx78650 Human PRO |
| 13 | 1473.6 | 98.3 | 1564 | 7 | ACA75622 | | | Aca75622 Novel hum |

| | | | | | | | | |
|----|--------|------|------|---|----------|--|--|--------------------|
| 14 | 1473.6 | 98.3 | 1564 | 7 | ACA71102 | | | Aca71102 Human sec |
| 15 | 1473.6 | 98.3 | 1564 | 7 | ACC87630 | | | Acc87630 Human sec |
| 16 | 1473.6 | 98.3 | 1564 | 7 | ACC87016 | | | Acc87016 Human sec |
| 17 | 1473.6 | 98.3 | 1564 | 7 | ACD04189 | | | AcD04189 Human sec |
| 18 | 1473.6 | 98.3 | 1564 | 7 | ACA69520 | | | AcA69520 cDNA enco |
| 19 | 1473.6 | 98.3 | 1564 | 7 | ACA90365 | | | AcA90365 Novel hum |
| 20 | 1473.6 | 98.3 | 1564 | 7 | ACC89472 | | | Acc89472 Human sec |
| 21 | 1473.6 | 98.3 | 1564 | 7 | ACA98263 | | | AcA98263 Novel hum |
| 22 | 1473.6 | 98.3 | 1564 | 7 | ACA93905 | | | AcA93905 Human sec |
| 23 | 1473.6 | 98.3 | 1564 | 7 | ACD15298 | | | AcD15298 Human sec |
| 24 | 1473.6 | 98.3 | 1564 | 7 | ACD08885 | | | AcD08885 Human sec |
| 25 | 1473.6 | 98.3 | 1564 | 7 | ACC96805 | | | Acc96805 Human sec |
| 26 | 1473.6 | 98.3 | 1564 | 7 | ACF15526 | | | AcF15526 Human sec |
| 27 | 1473.6 | 98.3 | 1564 | 7 | ACA72893 | | | AcA72893 Human PRO |
| 28 | 1473.6 | 98.3 | 1564 | 7 | ACD03065 | | | AcD03065 Novel hum |
| 29 | 1473.6 | 98.3 | 1564 | 7 | ACD01880 | | | AcD01880 Novel hum |
| 30 | 1473.6 | 98.3 | 1564 | 7 | ACA92072 | | | AcA92072 Novel hum |
| 31 | 1473.6 | 98.3 | 1564 | 7 | ACA89497 | | | AcA89497 cDNA enco |
| 32 | 1473.6 | 98.3 | 1564 | 7 | ACA73507 | | | AcA73507 Human sec |
| 33 | 1473.6 | 98.3 | 1564 | 7 | ACA05822 | | | AcA05822 Human sec |
| 34 | 1473.6 | 98.3 | 1564 | 7 | ACA66656 | | | AcA66656 cDNA enco |
| 35 | 1473.6 | 98.3 | 1564 | 7 | ACF20231 | | | AcF20231 Human sec |
| 36 | 1473.6 | 98.3 | 1564 | 7 | ACF19617 | | | AcF19617 Human sec |
| 37 | 1473.6 | 98.3 | 1564 | 7 | ACD21905 | | | AcD21905 Human sec |
| 38 | 1473.6 | 98.3 | 1564 | 7 | ACF13070 | | | AcF13070 Human sec |
| 39 | 1473.6 | 98.3 | 1564 | 7 | ACD25173 | | | AcD25173 Human sec |
| 40 | 1473.6 | 98.3 | 1564 | 7 | ACF00222 | | | AcF00222 Human sec |
| 41 | 1473.6 | 98.3 | 1564 | 7 | ACA72279 | | | AcA72279 Novel hum |
| 42 | 1473.6 | 98.3 | 1564 | 7 | ACD04803 | | | AcD04803 Novel hum |
| 43 | 1473.6 | 98.3 | 1564 | 7 | ACD18264 | | | AcD18264 Human sec |
| 44 | 1473.6 | 98.3 | 1564 | 7 | ACD08271 | | | AcD08271 Human sec |
| 45 | 1473.6 | 98.3 | 1564 | 7 | ACA88705 | | | AcA88705 Novel hum |

ALIGNMENTS

RESULT 1

AAF29357
ID AAF29357 standard; DNA; 1499 BP.
XX
AC AAF29357;
XX
XX
DI 20-APR-2001 (first entry)
XX
DE Amyloid-beta protein agglutination regulating factor DNA SEQ ID 1.
XX
KW Human; amyloid-beta protein; agglutination regulatory factor;
XX
KW Alzheimer's disease; ds.
XX
OS Homo sapiens.
XX
FN WO200104299-A1.
XX
PD 18-JAN-2001.
XX
PF 06-JUL-2000; 2000WO-JP004515.
XX
PR 08-JUL-1999; 99JP-00194179.
XX
PR 18-OCT-1999; 99US-0159586P.
XX
PA (HELI-) HELIX RES INST.
XX

PI Ota T, Isozaki T, Nishikawa T, Kawai Y, Yamazaki M, Satoh S;
 PI Arakawa H, Morita M;
 XX WPI; 2001-138347/14.
 DR P-PSDB; AAB49767.
 DR
 XX Polynucleotide encoding amyloid-beta protein agglutination-controlling
 PT factor, useful for inhibiting or promoting agglutination or sedimentation
 PT of amyloid-beta protein and in diagnosis and screening drugs for
 PT Alzheimer's disease.
 XX
 PS Claim 1; Page 43-45; 72pp; Japanese.
 XX
 CC This invention relates to polynucleotides AAF29357 ~ AAF29361 which
 CC encode proteins AAB49767 ~ AAB49771. The proteins inhibit or promote the
 CC agglutination of amyloid beta protein. The protein and polynucleotide
 CC sequences are useful in the diagnosis of Alzheimer's disease. They are
 CC also useful for screening drugs which are useful for treating Alzheimer's
 CC disease
 XX
 SQ Sequence 1499 BP; 293 A; 408 C; 430 G; 368 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1499; DB 4; Length 1499;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCTGACGCGGGCTTTAGGTGTCGGCTTTCCTGGCCGACGAAAGCTGATGAGCATG 60
 DB 1 GCGGCTGACGCGGGCTTTAGGTGTCGGCTTTCCTGGCCGACGAAAGCTGATGAGCATG 60
 QY 61 AAGCTCTATCTTTGGTGGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
 DB 61 AAGCTCTATCTTTGGTGGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
 QY 121 AAGGTTCTGAAGATTCGGTGCATATGCATCTGTCCACCTTATGAACATCAGTGGG 180
 DB 121 AAGGTTCTGAAGATTCGGTGCATATGCATCTGTCCACCTTATGAACATCAGTGGG 180
 QY 181 CATATTTACACCAAGAAATGTATCCAGAAAGGACTGCAACTGGCTGCAAGTACGAGTACGAG 240
 DB 181 CATATTTACACCAAGAAATGTATCCAGAAAGGACTGCAACTGGCTGCAAGTACGAGTACGAG 240
 QY 241 ATGCGAGTGGCTGGCCATGAGTGGAGGCTACTGCTGTGTGGAGTGCAGTACGAGTACGAG 300
 DB 241 ATGCGAGTGGCTGGCCATGAGTGGAGGCTACTGCTGTGTGGAGTGCAGTACGAGTACGAG 300
 QY 301 GAGCGCAGACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 360
 DB 301 GAGCGCAGACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 360
 QY 361 CTGTTGCTTACATGGCTTCTGATGCTGGTGGACCTCTGATCCGAAAGCCGATGCA 420
 DB 361 CTGTTGCTTACATGGCTTCTGATGCTGGTGGACCTCTGATCCGAAAGCCGATGCA 420
 QY 421 TACACTGAGCAACTGCACAAATGAGGAGGATGAGGATGCTGGCTCTATGCGAGCAGCT 480
 DB 421 TACACTGAGCAACTGCACAAATGAGGAGGATGAGGATGCTGGCTCTATGCGAGCAGCT 480
 QY 481 GCTGCATCCCTCGGGGACCCCGAGCAACACAGTCCCTGAGAGGCTGTGGAAGTGCACG 540
 DB 481 GCTGCATCCCTCGGGGACCCCGAGCAACACAGTCCCTGAGAGGCTGTGGAAGTGCACG 540
 QY 541 CAGGGTGGAGCTGCAGGTGCAGGAGCAGCGGAAGACATCTTGTGATCGGACACAGATG 600

DB 541 CAGGGTGGAGCTGCAGGTGCAGGAGCAGCGGAAGACAGTCTTGGATCGGACAGATG 630
 QY 601 CTACCTAGATGAGCTGGTGTGGTGGGTCAAGGCCCCCAACCAACCAACCAACCAACCAACCAAC 660
 DB 601 CTACCTAGATGAGCTGGTGTGGTGGGTCAAGGCCCCCAACCAACCAACCAACCAACCAACCAAC 660
 QY 661 AGGCTGACAAAGCAAGGGGCTACTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 720
 DB 661 AGGCTGACAAAGCAAGGGGCTACTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 720
 QY 721 GCTGTGGCAATTTTTCT 780
 DB 721 GCTGTGGCAATTTTTCT 780
 QY 781 TTAGGAAGAGGAGTGTGGTCTCTGATCT 840
 DB 781 TTAGGAAGAGGAGTGTGGTCTCTGATCT 840
 QY 841 GATGGGAG 900
 DB 841 GATGGGAG 900
 QY 901 CGATCTGTCT 960
 DB 901 CGATCTGTCT 960
 QY 961 TTACCTTTGGAAGATAAAGCTGGGTCTTCAGGAACCTCAGTGTCTGGGAGGAAGCATGGC 1020
 DB 961 TTACCTTTGGAAGATAAAGCTGGGTCTTCAGGAACCTCAGTGTCTGGGAGGAAGCATGGC 1020
 QY 1021 CAGCATTCAGCATGTGTCT 1080
 DB 1021 CAGCATTCAGCATGTGTCT 1080
 QY 1081 CAGCGCTCAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCC 1140
 DB 1081 CAGCGCTCAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCC 1140
 QY 1141 CCGCTTGAGCCCACTGGGTCTTCAAGGCTGCACTGGAAGCTGTGTCTGTCTCCCTGTGTG 1200
 DB 1141 CCGCTTGAGCCCACTGGGTCTTCAAGGCTGCACTGGAAGCTGTGTCTGTCTCCCTGTGTG 1200
 QY 1201 CACTTCTGCACTGGGCACTGGAGTGCCTGCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1260
 DB 1201 CACTTCTGCACTGGGCACTGGAGTGCCTGCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1260
 QY 1261 CACTTGAAGGCTGTGGGCACTGGGTCTTCAAGGCTGCACTGGAAGCTGTGTCTGTCTCCCTGTGTG 1320
 DB 1261 CACTTGAAGGCTGTGGGCACTGGGTCTTCAAGGCTGCACTGGAAGCTGTGTCTGTCTCCCTGTGTG 1320
 QY 1321 GTCGTTGGAACATGAGACTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1380
 DB 1321 GTCGTTGGAACATGAGACTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1380
 QY 1381 TGGGTTGCT 1440
 DB 1381 TGGGTTGCT 1440
 QY 1441 CTTGTCTTAGAGTTGTGTAAATCAAGGAAGCAATCATTAAATTTTATTCTCTC 1499
 DB 1441 CTTGTCTTAGAGTTGTGTAAATCAAGGAAGCAATCATTAAATTTTATTCTCTC 1499

RESULT 2
AAAF93749
ID AAF93749 standard; cDNA: 1499 BP.

XX
AC AAF93749;

XX
DT 23-MAY-2001 (first entry)

XX
DE Human cDNA encoding a membrane or

XX Human; secretory protein; membrane

XX
KW
rheumatoid arthritis; diabetes;
XX

US Homo sapiens.
XX
DN ED1067192-12

FN
XX
PD

07-JUL-2000: 2000EP-00114090.

08-JUL-1999; 99JP-00194179.

PR 11-JAN-2000; 2000JP-00118775.
PR C2-MAY-2000; 2000JP-00183766.

XX
PA (HELL-) HELIX RES INST.

XX
PI Ota T, Isogai T, Nishikawa T, I

XX.
DR WPI; 2001-093989/11.

DR P-PSDB; AAB0032Z.
XX
BT

PT gene therapy or as candidate target
PT nuclear acids encoding secretory
viral

PS Claim 1; SEQ ID NO 11; 609pp + Se
XX

CC This invention relates to nucleic
CC which encode human secretory or m

CC - AAB88419. Included in the inven
CC AAF622232 - AAF622235 which are use

CC invention. The invention also inc
CC antibodies directed against the p

CC be used in vaccines. The polynucle
CC therapy. The polynucleotide sequence

CC used in the prevention, treatment
CC with inappropriate secretory prot

CC nucleic acids and complementary s
CC in diagnostic assays (e.g. polymers

and quantitate the presence of si-
They may also be used to study the

CC proteins/membrane polypeptides and polypeptides may be used as antigens to elicit them and in assays to identify and/or detect them.

CC antagonists) of expression and ac
CC against chem and in assays to ind
CC may also be used as therapeutic a

may also be used as encephalitis activity. The antibodies may also detecting the presence of the pol

CC detecting the presence of anti-*Yersinia* antibodies

CC linked immunosorbent assay (ELISA)

CC treated include rheumatoid arthritis

Sequence 1499 BP; 293 A; 408 C; 4

| | |
|-----------|---|
| RESULT 2 | |
| AAAF93749 | |
| ID | AAF93749 standard; cDNA; 1499 BP. |
| XX | |
| XX | AAF93749; |
| AC | |
| DT | 23-MAY-2001 (first entry) |
| XX | |
| XX | Human cDNA encoding a membrane or secretory protein clone PSEC0012. |
| DE | |
| DE | Human; secretory protein; membrane protein; vaccine; gene therapy; AAS88317 |
| KW | rheumatoid arthritis; diabetes; ss. |
| KW | |
| XX | |
| XX | Homo sapiens. |
| OS | |
| XX | EF1067182-A2. |
| PN | |
| PN | 10-JAN-2001. |
| PD | |
| PD | 07-JUL-2000; 2000EP-00114090. |
| PF | |
| XX | |
| XX | 08-JUL-1999; 99JP-00194179. |
| PR | |
| PR | 11-JAN-2000; 2000JP-00118775. |
| PR | |
| PR | 02-MAY-2000; 2000JP-00183766. |
| XX | |
| XX | (HELI-) HELIX RES INST. |
| PA | |
| XX | |
| XX | Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K; |
| PI | |
| PI | WPI; 2001-093989/11. |
| DR | |
| DR | P-PSDB; AAB88322. |
| XX | |
| XX | Nucleic acids encoding secretory proteins/membrane proteins, useful in |
| PT | gene therapy or as candidate target molecules in drug development. |
| PT | |
| XX | Claim 1; SEQ ID NO 11; 609pp + Sequence Listing; English. |
| XX | |
| XX | This invention relates to nucleic acid sequences AAF93744 - AAF93916 |
| CC | which encode human secretory or membrane proteins represented by AAS88317 |
| CC | - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and |
| CC | AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the |
| CC | invention. The invention also includes methods for the production of |
| CC | antibodies directed against the proteins, and cDNA sequences, which can |
| CC | be used in vaccines. The polynucleotide sequences can be used in gene |
| CC | therapy. The polynucleotide sequences and the proteins they encode may be |
| CC | used in the prevention, treatment and diagnosis of diseases associated |
| CC | with inappropriate secretory protein/membrane protein expression. The |
| CC | nucleic acids and complementary sequences may also be used as DNA probes |
| CC | in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect |
| CC | and quantitate the presence of similar nucleic acid sequences in samples. |
| CC | They may also be used to study the expression and function of secretory |
| CC | proteins/membrane polypeptides and their role in metabolism. The |
| CC | polypeptides may be used as antigens in the production of antibodies |
| CC | against them and in assays to identify modulators (agonists and |
| CC | antagonists) of expression and activity. The antibodies and antagonists |
| CC | may also be used as therapeutic agents to down regulate expression and |
| CC | activity. The antibodies may also be used as diagnostic agents for |
| CC | detecting the presence of the polypeptides in samples (e.g. by enzyme |
| CC | linked immunosorbent assay (ELISA). Examples of diseases which may be |
| CC | treated include rheumatoid arthritis and diabetes |
| XX | |
| XX | Sequence 1499 BP; 293 A; 408 C; 430 G; 368 T; 0 U; 0 Other? |
| SO | |

```
/product= "transmembrane domain containing protein"
```

| | | | |
|----|-----|--|-----|
| QY | 121 | AAGAGTTCTGGAAGATATCCGGTGCAAATGCATCTGTCCACTTATGAAACATCAAGTGGG | 180 |
| DB | 126 | | 185 |
| QY | 181 | CATATTTCACCCAGAAATGTATCCGAGAGGACTGMACTGCCTGCACGTGTGTGGAGGCC | 240 |
| DB | 186 | | 245 |
| QY | 241 | ATGCCAGTGCCTCGCCATGACGTGGAGGCTACTGCTGTGTGGAGTTCGAGGTACGAG | 300 |
| DB | 246 | | 305 |
| QY | 301 | GAGCGKACACCCACCATCAAGGTCAATCTTCATCTAOCCTGCCTGTCGCTGGTGGTGGC | 360 |
| DB | 306 | | 365 |
| QY | 361 | CTGTTGCTTACATGGCCTTCCTGATGCTGGTGGACCTCTGATCCGAAAGCCGAGTSCA | 420 |
| DB | 366 | | 425 |

| | |
|----------|--|
| RESULT 3 | |
| AAV49584 | |
| ID | AAV49584 standard; cDNA to mRNA; 1504 BP. |
| XX | |
| XX | AAV49584; |
| XX | |
| XX | 21-OCT-1998 (first entry) |
| XX | |
| XX | Human stomach cancer cell clone Hpl0297 cDNA #1. |
| XX | |
| XX | Transmembrane domain; human; nutrition; cytokine; cell proliferation; |
| XX | differentiation; immune system; stimulator; suppressor; regulator; |
| XX | haematopoiesis; activin; inhibitor; chemotactic; chemokinetic; receptor; |
| XX | haemostatic; thrombolytic; ligand; anti-inflammatory; tumour; ds. |
| XX | |
| XX | Homo sapiens. |
| XX | |
| XX | Key |
| XX | Location/Qualifiers |
| XX | 63. .614 |
| XX | /*tag= a |
| FT | CDS |
| FT | FT |
| FT | FT |

| | | | |
|----------|-----------------------------------|---|------|
| D6 | 1326 | GTGGTTGGACACATGAGACTCGAGGCTGAGCGTGGGATCTGACACCAACAGCCCTGTACT | 1386 |
| QY | 1381 | TGGGTTGGCTCTTGTCCCTGAACATCGTTGTACAGTGCATGGAGAGAAAATTTGTCT | 1440 |
| D6 | 1386 | TGGGTTGGCTCTTGTCCCTGAACATCGCTTGTACAGTGCATGGAGAGAAAATTTGTCT | 1445 |
| QY | 1441 | CTTGTCTTAGAGTTGTGTGTAATCAAGGAAGCCATCATTAATTTGTTTATTTCTCTC | 1499 |
| D6 | 1446 | CTTGTCTTAGAGTTGTGTGTAATCAAGGAAGCCATCATTAATTTGTTTATTTCTCTC | 1504 |
| RESULT 4 | | | |
| ABV23182 | ABV23182 standard; cDNA; 1937 BP. | | |
| XX | ID | ABV23182 | |
| XX | AC | ABV23182; | |
| XX | DE | 16-SEP-2002 (first entry) | |
| XX | DE | Human prostate expression marker cDNA 23173. | |
| XX | DE | Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker; | |
| KW | KW | pharmacogenomic marker; gene; ss. | |
| KW | KW | | |
| OS | OS | Homo sapiens. | |
| OS | OS | | |
| PN | PN | WC200160860-A2. | |
| XX | XX | | |
| XX | XX | 23-AUG-2001. | |
| XX | XX | | |
| PF | PF | 20-FEB-2001; 2001WO-US00517L. | |
| XX | XX | | |
| PR | PR | 17-FEB-2000; 2000US-0183319P. | |
| PR | PR | 16-MAR-2000; 2000US-0189562P. | |
| PR | PR | 25-MAY-2000; 2000US-0207454P. | |
| PR | PR | 09-JUN-2000; 2000US-0211314P. | |
| PR | PR | 18-JUL-2000; 2000US-0219007P. | |
| PR | PR | 13-DEC-2000; 2000US-0255281P. | |
| PA | PA | (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC. | |
| XX | XX | | |
| PI | PI | Schlegel R, Endege WO, Monahan JZ; | |
| XX | XX | | |
| XX | XX | WPI; 2001-662795/76. | |
| XX | XX | | |
| PT | PT | Novel isolated nucleic acid molecule associated with cancerous state of | |
| PT | PT | prostate cells and correlating with presence of prostate cancer, useful | |
| PT | PT | for detecting presence of prostate cancer, stage of prostate cancer. | |
| XX | XX | | |
| XX | XX | Claim 1; Page 4163; 1175Opp; English. | |
| XX | XX | | |
| CC | CC | The invention relates to an isolated nucleic acid molecule (I) comprising | |
| CC | CC | a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the | |
| CC | CC | specification or its complement. (I) is useful for: (a) assessing whether | |
| CC | CC | a patient is afflicted with prostate cancer; (b) monitoring the | |
| CC | CC | progression of prostate cancer in a patient; (c) assessing the efficacy | |
| CC | CC | of a test compound to inhibit prostate cancer in a patient; (d) assessing | |
| CC | CC | the efficacy of a therapy for inhibiting prostate cancer in a patient; | |
| CC | CC | (e) selecting a composition for inhibiting prostate cancer in a patient; | |
| CC | CC | (f) assessing the prostate cell carcinogenic potential of a compound; (g) | |
| CC | CC | determining whether prostate cancer has metastasized in a patient; (h) | |
| CC | CC | assessing the aggressiveness or indolence of prostate cancer in a patient | |
| CC | CC | ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker | |

| | | |
|------|---|------|
| 421 | TACACTGAGCAACTGCACATGAGGAGAGAAATGAGGATGCTGCGCTCTATGGCAGCAGCT | 480 |
| QY | | |
| 426 | TACACTGAGCAACTGCACATGAGGAGAGAAATGAGGATGCTGCGCTCTATGGCAGCAGCT | 485 |
| DB | | |
| 481 | GCTGCATCCCTCGSGGGAGCCCGGACGCAAAAACAAGTCTTGAGGCGTGTGGAAAGTGCCGAG | 540 |
| QY | | |
| 486 | GCTGCATCCCTCGSGGGAGCCCGGACGCAAAAACAAGTCTTGAGGCGTGTGGAAAGTGCCGAG | 545 |
| DB | | |
| 541 | CAGCGGTGGAAAGCTTCGAGGTTCAGAGGACGCGGAGAGACATCTTCGATCGGCAACAAGTG | 600 |
| QY | | |
| 546 | CAGCGGTGGAAAGCTTCGAGGTTCAGAGGACGCGGAGAGACATCTTCGATCGGCAACAAGTG | 605 |
| DB | | |
| 601 | CTCAGCTAGATGGGCTGTGTGGTGTGGGTCAAGGCGCCCAACACCATGGCTGCCAGCTTCC | 660 |
| QY | | |
| 606 | CTCAGCTAGATGGGCTGTGTGGTGTGGGTCAAGGCGCCCAACACCATGGCTGCCAGCTTCC | 665 |
| DB | | |
| 661 | AGGCTGGACAAAAGAGGGGGGTACTTCTCCCTTCCTCGGTTCGAGCTTCCTCCCTTTAAAA | 720 |
| QY | | |
| 666 | AGGCTGGACAAAAGAGGGGGGTACTTCTCCCTTCCTCGGTTCGAGCTTCCTCCCTTTAAAA | 725 |
| DB | | |
| 721 | GCCTGTGGCAATTTTCTCCCTCTCCCTTACTTTAGAAATGTTGACTTGGCTATTTTGA | 780 |
| QY | | |
| 726 | GCCTGTGGCAATTTTCTCCCTCTCCCTTACTTTAGAAATGTTGACTTGGCTATTTTGA | 785 |
| DB | | |
| 781 | TTAGGAAAGAGGGATGTGGTCTCTGATCTCTGTTGTCTTTTGGGTCTTTGGGTTGAAG | 840 |
| QY | | |
| 786 | TTAGGAAAGAGGGATGTGGTCTCTGATCTCTGTTGTCTTTTGGGTCTTTGGGTTGAAG | 845 |
| DB | | |
| 841 | GGATGGGGAAGCGCAGGSCCAGAAAGGAATGGAGACATCGAGGCGGCTCAGAGATGGATG | 900 |
| QY | | |
| 846 | GGAGGGGGAGCGCAGGSCCAGAAAGGAATGGAGACATCGAGGCGGCTCAGAGATGGATG | 905 |
| DB | | |
| 901 | CGATCTGTCTCTCTGGCTCCACTCTTCCGCGGCTCCAGCTCTGAGTCTTGGGATGTG | 960 |
| QY | | |
| 906 | CGATCTGTCTCTCTGGCTCCACTCTTCCGCGGCTCCAGCTCTGAGTCTTGGGATGTG | 965 |
| DB | | |
| 961 | TTACCTTGGAAATAAAGCTGGGTTCTCAGGAACTCAGTGTCTGGAGGAAAAGCATGGC | 1020 |
| QY | | |
| 966 | TTACCTTGGAAATAAAGCTGGGTTCTCAGGAACTCAGTGTCTGGAGGAAAAGCATGGC | 1025 |
| DB | | |
| 1021 | CCAGCAATCAGCATGTGTTCTTTCTGCAATGGTTCCTTATCACAACCTCCCTCCAGGCC | 1080 |
| QY | | |
| 1026 | CCAGCAATCAGCATGTGTTCTTTCTGCAATGGTTCCTTATCACAACCTCCCTCCAGGCC | 1085 |
| DB | | |
| 1081 | CAGGGCTTCAGCCCAAGCCCAAGCTTCCAGCCCTGAGGACAGCTCTGATGGGAGCTGGG | 1140 |
| QY | | |
| 1086 | CAGGGCTTCAGCCCAAGCCCAAGCTTCCAGCCCTGAGGACAGCTCTGATGGGAGCTGGG | 1145 |
| DB | | |
| 1141 | CCCTCTTGAGCCCACTGGGTCTTCAGGGTGCACGTGGAAAGTGGTTCCTGTCCCTGTG | 1200 |
| QY | | |
| 1146 | CCCTCTTGAGCCCACTGGGTCTTCAGGGTGCACGTGGAAAGTGGTTCCTGTCCCTGTG | 1205 |
| DB | | |
| 1201 | CACCTTCCGCACTGGGGCAAGGAGTGGCCCAATGCATCTGCTGGCGGTCCCTTCACTG | 1260 |
| QY | | |
| 1206 | CACCTTCCGCACTGGGGCAAGGAGTGGCCCAATGCATCTGCTGGCGGTCCCTTCACTG | 1265 |
| DB | | |
| 1261 | CACCTTGAAGGGTCTGGGCAATTCCTCTCTCCCAAGTGTCCACAATCTGAGGCAAGAG | 1320 |
| QY | | |
| 1266 | CACCTTGAAGGGTCTGGGCAATTCCTCTCTCCCAAGTGTCCACAATCTGAGGCAAGAG | 1325 |
| DB | | |
| 1321 | GTCCGTTGGAAACATGAGACTCGAGGCTGAGCGTGGATCTGAACACCAAGCCCTGTACT | 1380 |
| QY | | |

XX SQ Sequence 1937 BP; 445 A; 510 C; 563 G; 399 T; 0 U; 23 Other;

Query Match 98.8%; Score 1481.6; DB 5; Length 1937;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1495; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 GGGGCTGACGGGCTGTAGGTGTCCGGCTTTGCTGGCCACGACAGCTGTATAGCATG 60
DB 120 GGGGCTGACGGGCTGTAGGTGTCCGGCTTTGCTGGCCACGACAGCTGTATAGCATG 179

QY 61 AGGCTCTATCTTTGGTGGCCGTGTCCGGCTTTGCTGGCCACGACAGCTGTATAGCATG 120
DB 180 AGGCTCTATCTTTGGTGGCCGTGTCCGGCTTTGCTGGCCACGACAGCTGTATAGCATG 239

QY 121 AGAGGCTCTGAATATCCGGTGCATATGCAATGCACTGTCCACCTTATAGAACATCACTGGG 180
DB 240 AGAGGCTCTGAATATCCGGTGCATATGCAATGCACTGTCCACCTTATAGAACATCACTGGG 299

QY 181 CATATTACAAACGAATGTATCCAGAAAGGACTGCACCTGCTGACGTGGTGGAGGCC 240
DB 300 CATATTACAAACGAATGTATCCAGAAAGGACTGCACCTGCTGACGTGGTGGAGGCC 359

QY 241 ATGCCAGTGCCTGGCCATGAGTGGAGGCTACTGCTGCTGGAGTGCAGTACGAG 300
DB 360 ATGCCAGTGCCTGGCCATGAGTGGAGGCTACTGCTGCTGGAGTGCAGTACGAG 419

QY 301 GAGCGACACACACACACACACAGGTCATCATTTGCTACCTGTCCTGGTGGTGGTGGC 360
DB 420 GAGCGACACACACACACACAGGTCATCATTTGCTACCTGTCCTGGTGGTGGTGGC 479

QY 361 CTGTTGCTCTACATGGCTTCTGATGCTGGTGGACCTCTGATCCGAAAGCCGATGCA 420
DB 480 CTGTTGCTCTACATGGCTTCTGATGCTGGTGGACCTCTGATCCGAAAGCCGATGCA 539

QY 421 TACACTGAGCAATGCAATGAGGAGGATGAGTGCCTGCTATGCGACAGCT 480
DB 540 TACACTGAGCAATGCAATGAGGAGGATGAGTGCCTGCTATGCGACAGCT 599

QY 481 GCTGCATCCCTCGGGGGACCCGACCAACACAGTCTGAGCGGTGTGGAAGTGGCCAG 540
DB 600 GCTGCATCCCTCGGGGGACCCGACCAACACAGTCTGAGCGGTGTGGAAGTGGCCAG 659

QY 541 CAGCGGTGGAAGCTGCAAGTGCAGGAGGACGCGGAGACAGTCTTCGATCGGACAGATG 600
DB 660 CAGCGGTGGAAGCTGCAAGTGCAGGAGGACGCGGAGACAGTCTTCGATCGGACAGATG 719

QY 601 CTCAGTAGATGGCTGGTGTGGTGGTCAAGGCCACACACACAGTGGTGGTGGTGGTGG 660
DB 720 CTCAGTAGATGGCTGGTGTGGTGGTCAAGGCCACACACAGTGGTGGTGGTGGTGG 779

QY 661 AGGCTGGACAAAGCAAGGGGGTACTTCTCCCTTCCCTGGTTCAGTCTTCCCTTAAAA 720
DB 780 AGGCTGGACAAAGCAAGGGGGTACTTCTCCCTTCCCTGGTTCAGTCTTCCCTTAAAA 839

QY 721 GCTGTGGCATTTTCTCCTCTCTCCTTACCTTACCTTACCTTACCTTACCTTACCTT 780
DB 840 GCTGTGGCATTTTCTCCTCTCTCCTTACCTTACCTTACCTTACCTTACCTTACCTT 899

QY 781 TTAGGGAAGAGGAGTGGTGTCTGATCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTCTG 840
DB 900 TTAGGGAAGAGGAGTGGTGTCTGATCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTCTG 959

QY 841 GGTGGGGAAGGCGAGGCCAGAGGGGATGAGACATTGAGGGGGGCTTCAGGAGTGGATG 900
DB 960 GGAAGGGGAAGGCGAGGCCAGAGGGGATGAGACATTGAGGGGGGCTTCAGGAGTGGATG 1019

QY 901 CGATCTGCTCTCTCTGGCTCCACTCTTCCGGCTTCCAGCTCTGAGCTCTTGGGAATGTTG 960
DB 1020 CGATCTGCTCTCTCTGGCTCCACTCTTCCGGCTTCCAGCTCTGAGCTCTGGAATGTTG 1079

QY 961 TTACCCCTTGAAGATAAAGCTGGGCTTTCAGGAACCTCAGTGTCTGAGGAAGAAGATGGC 1020
DB 1080 TTACCCCTTGAAGATAAAGCTGGGCTTTCAGGAACCTCAGTGTCTGAGGAAGAAGATGGC 1139

QY 1021 CCAGCATTCAGCATGTGTTCCCTTCTGCACTGGTTC-TTATCACCACTCCCTCCAGAC 1079
DB 1140 CCAGCATTCAGCATGTGTTCCCTTCTGCACTGGTTC-TTATCACCACTCCCTCCAGAC 1199

QY 1080 CCAGCGCTCAGCCGCCAGCCAGCTCCAGCGCTTCCAGCGCTCTGATGGAGAGCTGG 1139
DB 1200 CCAGCGCTCAGCCGCCAGCCAGCTCCAGCGCTTCCAGCGCTCTGATGGAGAGCTGG 1259

QY 1140 GCGCCCTGAGCCACTGGGCTTTCAGGGTGCATGGAGCTGGTGTGCTGTCCCTGT 1199
DB 1260 GCGCCCTGAGCCACTGGGCTTTCAGGGTGCATGGAGCTGGTGTGCTGTCCCTGT 1319

QY 1200 GCATCTCTGCACTGGGCTGAGTGGCCATGCACTCTCTGCGGGTCCCTCACCT 1259
DB 1320 GCATCTCTGCACTGGGCTGAGTGGCCATGCACTCTCTGCGGGTCCCTCACCT 1379

QY 1260 GCATCTGAGGGGTGGGCGAGTCCCTCCCTCTCCCGAGTCCAGCTACTGAGCGAGAC 1319
DB 1380 GCATCTGAGGGGTGGGCGAGTCCCTCCCTCTCCCGAGTCCAGCTACTGAGCGAGAC 1439

QY 1320 GGTGGTGGAACTGAGCTCGAGGCTGAGGCTGAGTGGAACTGAAACCCAGAGCCCTGTAC 1379
DB 1440 GGTGGTGGAACTGAGCTCGAGGCTGAGGCTGAGTGGAACTGAAACCCAGAGCCCTGTAC 1499

QY 1380 TTGGGTTGCTCTGTTCCCTGAACTTCTGCTACAGTGCATGGAGAGAAATTTGTC 1439
DB 1500 TTGGGTTGCTCTGTTCCCTGAACTTCTGCTACAGTGCATGGAGAGAAATTTGTC 1559

QY 1440 TCTGCTTGAAGTGTGTGTAAATCAAGGAAGCCATCAATTAATTTGTTTTCCTC 1499
DB 1560 TCTGCTTGAAGTGTGTGTAAATCAAGGAAGCCATCAATTAATTTGTTTTCCTC 1619

RESULT 5
AAF21831 standard; DNA; 1645 BP.

XX AAF21831;

XX 27-MAR-2001 (first entry)

Human breast and ovarian cancer associated antigen gene SEQ ID 218.
Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
zootropic; neurprotection; antiviral; antiallergic; hepatotropic;
antidiabetic; antiinflammatory; antitumor; vulnery; anticonvulsant;
antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
Addison's disease; allergy; autoimmune haemolytic anaemia;
autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
cardiovascular disorder; wound healing; neurological disease; ds.

XX OS Homo sapiens.
 XX EN WO2005173-A1.
 XX PD 21-SEP-2000.
 XX PF 08-MAR-2000; 2000WO-US05881.
 XX PR 12-MAR-1999; 99US-0124270P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Rosen CA, Ruben SM;
 XX DR WPI; 2000-611515/58.
 XX PI P-PSDB; AAB58928.
 XX PT New human breast and ovarian cancer associated gene sequences and the
 PT polypeptides encoded by these genes, useful in the prevention, treatment
 PT and diagnosis of cancer, immune disorders, cardiovascular disorders and
 PT neurological diseases.
 XX PS Claim 1; Page 645-646; 1299pp; English.
 XX CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
 CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
 CC associated with breast and ovarian cancer. Included in the invention are
 CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
 CC isolation and characterisation of the DNA and protein sequences of the
 CC invention. The breast and ovarian cancer associated DNA, protein, agonist
 CC or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic;
 CC neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic;
 CC antiinflammatory; antitumor; anticonvulsant; antibacterial;
 CC antifungal; antiparasitic and cardiant activity. The polynucleotide and
 CC protein sequences are used in the diagnosis of cancer, particularly
 CC breast and ovarian cancer. The nucleic acid sequences, proteins, agonists
 CC and agonists may also be used in the diagnosis, prevention and treatment
 CC of immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
 CC cardiovascular disorders such as myocardial ischaemias; wound healing;
 CC neurological diseases such as cerebral anoxia and epilepsy; and
 CC infectious diseases
 XX SQ Sequence 1645 BP; 400 A; 419 C; 448 G; 374 T; 0 U; 4 Other;

Query Match 98.8%; Score 1481.4; DB 3; Length 1645;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 1493; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Qy 1 GCGGCTGCAGGGGCTTGTAGGTGTCCGGCTTTGCTGGCCAGCAAGCCTGATAGCATG 60
 Db 39 GCGGCTGCAGGGGCTTGTAGGTGTCCGGCTTTGCTGGCCAGCAAGCCTGATAGCATG 98
 Qy 61 AGCTCTTATCTTGTGGGCTGTGGGCTTTGCTGGCCAGCAAGCCTGATAGCATG 120
 Db 99 AGCTCTTATCTTGTGGGCTGTGGGCTTTGCTGGCCAGCAAGCCTGATAGCATG 158
 Qy 121 AAGAGTCTGAAGATACCGGTGCAATGCATCTGTCCACTATAGAAACATCAGTGG 180
 Db 159 AAGAGTCTGAAGATACCGGTGCAATGCATCTGTCCACTATAGAAACATCAGTGG 218

Qy 181 CATATTTACACCAAGATGTATCCCAAGAGACTGCNACTGCCTGCAGCTGTGGAGCCC 240
 Db 219 CACATTTACACCAAGATGTATCCCAAGAGACTGCNACTGCCTGCAGCTGTGGAGCCC 278
 Qy 241 ATGCCAGTGCCTGGCCATGACCTGGAGGCTTACTGCCTGCTGTGGAGTGCAGGTACGAS 300
 Db 279 ATGCCAGTGCCTGGCCATGACCTGGAGGCTTACTGCCTGCTGTGGAGTGCAGGTACGAS 338
 Qy 301 GAGGCGACACCAACCACTCAAGGTCAATCATTTGTCATCTAOCCTGTCCGTGGTGGTGGC 360
 Db 339 GAGGCGACACCAACCACTCAAGGTCAATCATTTGTCATCTAOCCTGTCCGTGGTGGTGGC 398
 Qy 361 CTGTGCTCTTACATGGCTTCTGTGATGCTGGTGGACCTCTGATCCGAAGCCGGATGCA 420
 Db 399 CTGTGCTCTTACATGGCTTCTGTGATGCTGGTGGACCTCTGATCCGAAGCCGGATGCA 458
 Qy 421 TACACTGAGCAACTGCACATGAGGAGGAGATGAGGATGCTCGCTCTATGGCAGAGCT 480
 Db 459 TAYACTGAGCAACTGCACATGAGGAGGAGATGAGGATGCTCGCTCTATGGCAGAGCT 518
 Qy 481 GCTGCATCCCTCGGGGGACCCCGAACAACAACAGTCTCGAGGCTGTGAAAGGTGGCCAG 540
 Db 519 GCTGCATCCCTCGGGGGACCCCGAACAACAACAGTCTCGAGGCTGTGAAAGGTGGCCAG 578
 Qy 541 CAGGCTGGAAGCTGCAGGTGCAGGAGCAAGGAGACAGTCTTCGATCCGCAACAGATG 600
 Db 579 CAGGCTGGAAGCTGCAGGTGCAGGAGCAAGGAGACAGTCTTCGATCCGCAACAGATG 638
 Qy 601 CTCAGCTAGATGGGCTGGTGTGCTTGGGTCAAGGCCCAACACACATGGTGGCAGCTTCC 660
 Db 639 CTCAGCTAGATGGGCTGGTGTGCTTGGGTCAAGGCCCAACACACATGGTGGCAGCTTCC 698
 Qy 661 AGGCTGAGCAAGAGAGGGGCTACTTCTCCCTCCCTCGGTTCAGTCTTCCCTTTAAA 720
 Db 699 AGGCTGAGCAAGAGAGGGGCTACTTCTCCCTCCCTCGGTTCAGTCTTCCCTTTAAA 758
 Qy 721 GCTGTGGCAATTTTCTCTCTTCTCCCTTCTCCCTTCTAGAAATGTGTACTTGGCTATTTGA 780
 Db 759 GCTGTGGCAATTTTCTCTCTTCTCCCTTCTCCCTTCTAGAAATGTGTACTTGGCTATTTGA 818
 Qy 781 TTAGGGAAGAGGAGTGTGGTCTCTGATCTGTGTGTCTTGGGTCTTTGGGTTGAAG 840
 Db 819 TTAGGGAAGAGGAGTGTGGTCTCTGATCTGTGTGTCTTGGGTCTTTGGGTTGAAG 878
 Qy 841 GATGGGGAAGGAGGAGGAGGAGGAGATGGAGACATTCAGGCGGCTCAGGAGTGGATG 900
 Db 879 GATGGGGAAGGAGGAGGAGGAGGAGATGGAGACATTCAGGCGGCTCAGGAGTGGATG 938
 Qy 901 CGATCTGTCTCTCTGGCTCCACTCTTGGCGCTTCCAGCTCTGAGTCTTGGAAATGTG 960
 Db 939 CGATCTGTCTCTCTGGCTCCACTCTTGGCGCTTCCAGCTCTGAGTCTTGGAAATGTG 998
 Qy 961 TTAOCCTTGGAGATAAAGCTGGGCTTTTCAAGAACTCAGTGTGGAGGAAGCATGGC 1020
 Db 999 TTAOCCTTGGAGATAAAGCTGGGCTTTTCAAGAACTCAGTGTGGAGGAAGCATGGC 1058
 Qy 1021 CCAGCATTCAGCATGTGTCTTCTTTCGAGTGGTTC-TTATCAACCTCCCTCCAGGC 1079
 Db 1059 CCAGCATTCAGCATGTGTCTTCTTTCGAGTGGTTC-TTATCAACCTCCCTCCAGGC 1118
 Qy 1080 CCAGGCTCTCAGGCCCCCAGGCCAGCTCCAGGCTTGAAGGAGGAGTCTGAGGAGGAGTGG 1139
 Db 1119 CCAGGCTCTCAGGCCCCCAGGCCAGCTCCAGGCTTGAAGGAGGAGTCTGAGGAGGAGTGG 1178

QY 1140 GCCCCTGAGCCCACTGGGCTCTTCAGGGTGCACCTGGAGCTGGTGTTCGGTCTCCCTGT 1199
 D 1179 GCGCCCTGAGCCCACTGGGCTCTTCAGGGTGCACCTGGAGCTGGTGTTCGGTCTCCCTGT 1238
 QY 1200 GCACTCTGCACTGGGCTGGAGTGGCAATGCACTCTGCTGGCGTCCCTTCACCT 1259
 D 1239 GCACTCTGCACTGGGCTGGAGTGGCAATGCACTCTGCTGGCGTCCCTTCACCT 1298
 QY 1260 GCACTTGAGGGGCTCTGGGCTGGAGTGGCAATGCACTCTGCTGGCGTCCCTTCACCT 1319
 D 1299 GCACTTGAGGGGCTCTGGGCTGGAGTGGCAATGCACTCTGCTGGCGTCCCTTCACCT 1358
 QY 1320 GGTGGTGGAGCTGAGCTGGAGTGGCAATGCACTCTGCTGGCGTCCCTTCACCT 1379
 D 1359 GGTGGTGGAGCTGAGCTGGAGTGGCAATGCACTCTGCTGGCGTCCCTTCACCT 1418
 QY 1380 TTGGTGGTGGAGCTGAGCTGGAGTGGCAATGCACTCTGCTGGCGTCCCTTCACCT 1439
 D 1419 TTGGTGGTGGAGCTGAGCTGGAGTGGCAATGCACTCTGCTGGCGTCCCTTCACCT 1478
 QY 1440 TCTGTCTTGAAGTGTGTGTAAATCAGGAAGCCATCAATTAATTTTATTTCTC 1499
 D 1479 TCTGTCTTGAAGTGTGTGTAAATCAGGAAGCCATCAATTAATTTTATTTCTC 1538

RESULT 6

ID ABQ91986
 XX ABQ91986 standard; cDNA; 1562 BP.
 AC ABQ91986;
 XX
 DT 30-SEP-2002 (first entry)
 XX
 DE Human NF-kB activating gene SEQ ID NO 150.
 XX
 KW Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;
 KW immunomodulator; cytostatic; antineoplastic; osteopontin; neotropic;
 KW neuroprotective; anti-HIV; autoimmune disease; cancer; infection;
 KW bone disease; AIDS; neurodegenerative disease; ischaemic disorder; gene;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 XX
 PN WO200253737-A1.
 XX
 PD 11-JUL-2002.
 XX
 XX
 PF 25-DEC-2001; 2001WO-JP011389.
 XX
 XX
 PR 28-DEC-2000; 2000JP-00402288.
 PR 26-MAR-2001; 2001JP-00088912.
 PR 24-AUG-2001; 2001JP-00254018.
 XX
 XX (ASAH) ASAHI KASEI KOGYO KK.
 XX
 XX
 PI Matsuda A, Honda G, Muramatsu S, Nagano Y;
 XX
 DR WPI; 2002-583617/62.
 DR P-PSDB; ABP61498.
 XX
 XX NF-approximatelykB activating gene and expressed protein, applicable in
 PT diagnosis and screening inhibitors or promoters to control excessive
 PT

PT activation or inhibition for treating e.g. inflammations, autoimmune
 diseases and cancer.
 XX
 PS Claim 4; Page 641-644; 841pp; Japanese.
 XX
 CC The invention relates to a purified protein (I), comprising one of 90
 CC fully defined sequences (ABP61424-ABP61513) or a protein based on any of
 CC the sequences but with some amino acids deleted, substituted or added and
 CC with a NF-kB (nuclear factor kappa B) activating effect. The protein and
 CC encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening
 CC inhibitors or promoters to control excessive activation or inhibition and
 CC for treating e.g. inflammations, autoimmune diseases, cancers,
 CC infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic
 CC disorders
 XX
 SQ Sequence 1562 BP; 310 A; 417 C; 457 G; 378 T; 0 U; 0 Other;
 Query Match 98.7%; Score 1480; DB 6; Length 1562;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1494; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
 QY 1 GCGGCTGAGCGGGCTTGTAGGTGTGCGGCTTTGTGTCGCCAGCAAGCTGTATAGCATG 60
 D 63 GCGGCTGAGCGGGCTTGTAGGTGTGCGGCTTTGTGTCGCCAGCAAGCTGTATAGCATG 122
 QY 61 AAGCTCTATCTTTGGTGGCGGTGTGCGGTGTTTGTGTTGTCGCCAGCTGAGCCATG 120
 D 123 AAGCTCTATCTTTGGTGGCGGTGTGCGGTGTTTGTGTTGTCGCCAGCTGAGCCATG 182
 QY 121 AAGAGTCTTGAAGATATCCGGTGCMAATGCACTCTGTCCACCTTATAGAAACATCACTGGG 180
 D 183 AAGAGTCTTGAAGATATCCGGTGCMAATGCACTCTGTCCACCTTATAGAAACATCACTGGG 242
 QY 181 CATATTACAAACAGAAATGATCCCAAGAGGACTGCACTGCTGCAAGCTGTGAGCC 240
 D 243 CACATTTACAAACAGAAATGATCCCAAGAGGACTGCACTGCTGCAAGCTGTGAGCC 302
 QY 241 ATGCCAGTGGCTGGCCATGAGTGGAGGCTACTGCTGCTGTGCGAGTGCAGGTAGAG 300
 D 303 ATGCCAGTGGCTGGCCATGAGTGGAGGCTACTGCTGCTGTGCGAGTGCAGGTAGAG 362
 QY 301 GAGCGAGCAACCAACCATCAAGGTCTCATTTGTCTATCTACTGTCTGCTGGTGGTGGC 360
 D 363 GAGCGAGCAACCAACCATCAAGGTCTCATTTGTCTATCTACTGTCTGCTGGTGGTGGC 422
 QY 361 CTGTTGCTCTACATGGCCTTCTGATGCTGGTGGAGCTCTGATCCGAAAGCCGATGCA 420
 D 423 CTGTTGCTCTACATGGCCTTCTGATGCTGGTGGAGCTCTGATCCGAAAGCCGATGCA 482
 QY 421 TACACTGAGCACTGCAATGAGGAGGAGAAATGAGATGCTGCTCTATGCGACGAGCT 480
 D 483 TATACTGAGCACTGCAATGAGGAGGAGAAATGAGATGCTGCTCTATGCGACGAGCT 542
 QY 481 GCTGCATCCCTCGGGGGACCCCGAGCAAAACACAGTCTCTGAGCGTGTGAGAGTGGCCAG 540
 D 543 GCTGCATCCCTCGGGGGACCCCGAGCAAAACACAGTCTCTGAGCGTGTGAGAGTGGCCAG 602
 QY 541 CAGCGGTGGAAGCTGCAAGTGCAGGAGCAAGCGGAGACAGCTCTTCGATCGGCAAGATG 600
 D 603 CAGCGGTGGAAGCTGCAAGTGCAGGAGCAAGCGGAGACAGCTCTTCGATCGGCAAGATG 662
 QY 601 CTCAGCTAGATGGCTGTGTGTTGGTCAAGGCCCCCAACACCATGGCTGCCAGCTTCC 660

| | | |
|----|---|--|
| AC | AA039939; | |
| XX | 16-OCT-2000 (first entry) | |
| XX | Human TANGO 183 cDNA. | |
| XX | TANGO 180; TANGO 181; TANGO 182; TANGO 183; TANGO 184; TANGO 185; | |
| XX | TANGO 186; TANGO 188; TANGO 189; TANGO 215; TANGO 187; human; murine; | |
| XX | secreted protein; transmembrane protein; gene therapy; vaccine; | |
| XX | diagnosis; treatment; detection; ss. | |
| XX | Hom sapiens. | |
| XX | Key Location/Qualifiers | |
| XX | CDS 96..647 | |
| XX | FT /+tag= a | |
| XX | FT /product= "TANGO 183" | |
| XX | W0200018904-A2. | |
| XX | 06-APR-2000. | |
| XX | 30-SEP-1999; 99WO-US022817. | |
| XX | 30-SEP-1998; 98US-00164220. | |
| XX | 02-OCT-1998; 98US-00164169. | |
| XX | (MILL-) MILLENNIUM BIOTHERAPEUTICS INC. | |
| XX | Barnes TM; | |
| XX | WPI; 2000-2933144/25. | |
| XX | P-PSDB; AAY88274. | |
| XX | Isolated nucleic acids encoding TANGO polypeptides useful for preventing, | |
| XX | diagnosing and treating diseases associated with inappropriate protein | |
| XX | expression. | |
| XX | Claim 1c; Fig 7; 249pp; English. | |
| XX | This invention describes novel human and murine nucleic acids encoding | |
| XX | TANGO polypeptides (which are either wholly secreted or transmembrane | |
| XX | proteins) which can be used for gene therapy and/or vaccination. The | |
| XX | peptides are designated TANGO 180 to TANGO 189 and TANGO 215. The nucleic | |
| XX | acids may be used to produce TANGO 180 to TANGO 189 and TANGO 215 | |
| XX | polypeptides according to standard recombinant DNA methodologies. They | |
| XX | may also be used to detect and quantify the presence of TANGO nucleic | |
| XX | acids in a sample and therefore identify or diagnose diseases associated | |
| XX | with inappropriate TANGO expression (e.g. diseases related to over or | |
| XX | under expression of the polypeptides or the expression of inactive | |
| XX | polypeptides). The nucleic acids and the polypeptides they encode may be | |
| XX | used according to standard gene therapy protocols, to treat diseases | |
| XX | associated with inappropriate TANGO expression by supplementing a | |
| XX | patients own production of the polypeptide of to rectify mutations that | |
| XX | may result in expression of an abnormally active polypeptide. The | |
| XX | polypeptides may also be used to identify and produce agonists and | |
| XX | antagonists of TANGO expression and activity which may be used to | |
| XX | modulate TANGO related processes and diseases. The polypeptides are | |
| XX | particularly useful for use as antigens for producing antibodies to TANGO | |
| XX | proteins which may be used for inhibiting the activity of TANGO proteins. | |
| XX | They may also be used to detect and quantify the presence of TANGO | |
| XX | proteins in samples and therefore identify patients in whom the protein | |
| XX | is over- or under-expressed. This sequence encodes the human TANGO 183 | |

CC particularly useful for use as antigens for producing antibodies to TANGO proteins.
CC
CC proteins which may be used for inhibiting the activity of TANGO proteins.
CC They may also be used to detect and quantify the presence of TANGO
CC proteins in samples and therefore identify patients in whom the protein
CC is over- or under-expressed. This sequence encodes the human TANGO 183

XX 18-AUG-2000; 2000WO-IB001496.
 XX PF
 XX 18-AUG-1999; 99US-0149499P.
 PR PR
 XX 28-SEP-1999; 99US-0156503P.
 XX PA
 XX (GEHU-) GERMAN HUMAN GENOME PROJECT.
 XX WIemann S;
 P1
 XX WPI; 2001-327840/34.
 DR P-PSDB; ABUS2631.
 XX
 PT Nucleic acids having the sequences of clones isolated from libraries of
 PT different human tissues, useful in recombinant DNA methodologies.
 XX
 PS Claim 1; Page 144; 1095pp; English.
 XX
 CC This invention describes novel polynucleotides and polypeptides isolated
 CC from human cDNA libraries which can be used for gene therapy or in
 CC vaccines. The polynucleotides of the invention and antibodies encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate polypeptide expression. The products of the
 CC invention may also be used to identify modulators of expression and
 CC activity and to down regulate expression and activity. The antibodies of
 CC the invention may also be used as diagnostic agents for detecting the
 CC presence of polypeptides in samples. This sequence encodes a polypeptide
 CC described in the disclosure of the invention
 XX
 SQ Sequence 1552 BP; 318 A; 412 C; 444 G; 378 T; 0 U; 0 Other;

Query Match 98.4%; Score 1475; DB 5; Length 1552;

Best Local Similarity 99.3%; Pred. No. 0;
 Matches 1494; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

QY 1 GGGGCTGCAGGGGGCTTTAGGTGTGGGCTTTGGTGGCCAGCAAGCTGTATAGCATG 60
 DB |||||
 QY 24 GGGGCTGCAGGGGGCTTTAGGTGTGGGCTTTGGTGGCCAGCAAGCTGTATAGCATG 83
 DB |||||
 QY 61 AAGCTCTTATCTTTGGTGGGCTTTGGTGGGCTTTGGTGGGCTTTGGTGGGCTTTGGTGGG 120
 DB |||||
 QY 84 AAGCTCTTATCTTTGGTGGGCTTTGGTGGGCTTTGGTGGGCTTTGGTGGGCTTTGGTGGG 143
 DB |||||
 QY 121 AAGGTTCTGAAGATTCGGGTGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 180
 DB |||||
 QY 144 AAGGTTCTGAAGATTCGGGTGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 203
 DB |||||
 QY 181 CATATTACACCAAGATGTATCCAGAGGACT-----GCAACTGCTGCAAGTGGTG 234
 DB |||||
 QY 204 CACATTTACACCAAGATGTATCCAGAGGACTTTGTATGCAACTGCTGCAAGTGGTG 263
 DB |||||
 QY 235 GAGCCATGCAAGTGGGCTTTGGTGGGCTTTGGTGGGCTTTGGTGGGCTTTGGTGGGCTTTGG 294
 DB |||||
 QY 264 GAGCCATGCAAGTGGGCTTTGGTGGGCTTTGGTGGGCTTTGGTGGGCTTTGGTGGGCTTTGG 323
 DB |||||
 QY 295 TAGGAGGCGGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 354
 DB |||||
 QY 324 TAGGAGGCGGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 383
 DB |||||
 QY 355 GGTGGCCTTTGTCTTACATGGGCTTTCTCATGTGGTGGGCTTTCTCATGTGGTGGGCTTTCT 414
 DB |||||
 QY 384 GGTGGCCTTTGTCTTACATGGGCTTTCTCATGTGGTGGGCTTTCTCATGTGGTGGGCTTTCT 443
 DB |||||

QY 415 GATGCATACACTGAGCAACTGCACAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 474
 DB |||||
 QY 444 GATGCATACACTGAGCAACTGCACAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 503
 DB |||||
 QY 475 GCAGCTGCTGCATCCCTGGGGGAGCCCGAGCAAAACACAGTCTCTGGAGGCTGTGGAGGT 534
 DB |||||
 QY 504 GCAGCTGCTGCATCCCTGGGGGAGCCCGAGCAAAACACAGTCTCTGGAGGCTGTGGAGGT 563
 DB |||||
 QY 535 GCGCAGCAGCGGTGGAAGCTGCAGGTGCAAGGAGCGGAAAGACAGTCTTTCGATCGGCAC 594
 DB |||||
 QY 564 GCGCAGCAGCGGTGGAAGCTGCAGGTGCAAGGAGCGGAAAGACAGTCTTTCGATCGGCAC 623
 DB |||||
 QY 595 AAGATGCTCAGCTAGATGGGCTGGTGTGGTGGTTCAGGCGCCCAACACAGTCTTTCGATCGGC 654
 DB |||||
 QY 624 AAGATGCTCAGCTAGATGGGCTGGTGTGGTGGTTCAGGCGCCCAACACAGTCTTTCGATCGGC 683
 DB |||||
 QY 655 GCTTCCAGGCTGCACAAAGCAGGGGCTTCTCTCCCTTCCCTGGTTCAGGCTTTCCTCT 714
 DB |||||
 QY 684 GCTTCCAGGCTGCACAAAGCAGGGGCTTCTCTCCCTTCCCTGGTTCAGGCTTTCCTCT 743
 DB |||||
 QY 715 TTAAGGCTGTGGGCAATTTTCTCTCTCCCTTACTTTAGAAATGTGTACTTGGCTA 774
 DB |||||
 QY 744 TTAAGGCTGTGGGCAATTTTCTCTCTCCCTTACTTTAGAAATGTGTACTTGGCTA 803
 DB |||||
 QY 775 TTTGATTAGGGAAGCAGGGAGTGTGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 834
 DB |||||
 QY 804 TTTGATTAGGGAAGCAGGGAGTGTGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 863
 DB |||||
 QY 835 TTGAAGGAGTGGGGAAGCAGGGAGTGTGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 894
 DB |||||
 QY 864 TTGAAGGAGGGAAGCAGGGAGTGTGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 923
 DB |||||
 QY 895 TGGATGAGATCTGTCTCTCTGGCTCCACTCTTGGCGGCTTCCAGCTCTGAGTCTTGGGA 954
 DB |||||
 QY 924 TGGATGAGATCTGTCTCTCTGGCTCCACTCTTGGCGGCTTCCAGCTCTGAGTCTTGGGA 983
 DB |||||
 QY 955 ATGTTGTACCTTGGAAAGATAAAGCTGGGTCTTCAAGAACTCAGTGTCTGGGAGGAAG 1014
 DB |||||
 QY 984 ATGTTGTACCTTGGAAAGATAAAGCTGGGTCTTCAAGAACTCAGTGTCTGGGAGGAAG 1043
 DB |||||
 QY 1015 CATGGCCCAAGTTCAGCATGTGTCTCTCTCTGGAGTGGTCTTATCAACAAGCTTCCCTCC 1074
 DB |||||
 QY 1044 CATGGCCCAAGTTCAGCATGTGTCTCTCTCTGGAGTGGTCTTATCAACAAGCTTCCCTCC 1103
 DB |||||
 QY 1075 CAGCCCAAGGCTTCAGCCCAAGCTCCAGCTCCAGGCTGAGGACAGCTCTGATGGAGA 1134
 DB |||||
 QY 1104 CAGCCCAAGGCTTCAGCCCAAGCTCCAGGCTGAGGACAGCTCTGATGGAGA 1163
 DB |||||
 QY 1135 GCTGGGCGGCTTCAGCCCAAGCTGGGTCTTCAAGGCTGCACTGGAAAGCTGTGTCTGGTGT 1194
 DB |||||
 QY 1164 GCTGGGCGGCTTCAGCCCAAGCTGGGTCTTCAAGGCTGCACTGGAAAGCTGTGTCTGGTGT 1223
 DB |||||
 QY 1195 CTTGTGCACTTCGCACTGGGCACTGGAGTGGGCACTGGGCACTGGGCACTGGGCACTGGGCACT 1254
 DB |||||
 QY 1224 CTTGTGCACTTCGCACTGGGCACTGGAGTGGGCACTGGGCACTGGGCACTGGGCACTGGGCACT 1283
 DB |||||
 QY 1255 CACTGCACTTCGAGGCTGGGCACTGGGCACTGGGCACTGGGCACTGGGCACTGGGCACTGGGCA 1314
 DB |||||
 QY 1284 CACTGCACTTCGAGGCTGGGCACTGGGCACTGGGCACTGGGCACTGGGCACTGGGCACTGGGCA 1343
 DB |||||
 QY 1315 CAGAGGCTGGGCACTGGGCACTGGGCACTGGGCACTGGGCACTGGGCACTGGGCACTGGGCACT 1374
 DB |||||
 QY 1344 CAGAGGCTGGGCACTGGGCACTGGGCACTGGGCACTGGGCACTGGGCACTGGGCACTGGGCACT 1403
 DB |||||

| | | | | | | |
|----------|---|---|------|----|--------------|----------------|
| QY | 1375 | TGTACTGGGTGGCTCTTGTCCTCGTGAACCTTGTTTACCAATGTCATGGAGAGAAATTT | 1434 | PR | 17-SEP-1998; | 98US-0100684P; |
| | | | | PR | 17-SEP-1998; | 98US-0100710P; |
| Db | 1404 | TGTACTGGGTGGCTCTTGTCCTCGTGAACCTTGTTTACCAATGTCATGGAGAGAAATTT | 1463 | PR | 17-SEP-1998; | 98US-0100919P; |
| | | | | PR | 17-SEP-1998; | 98US-0100930P; |
| QY | 1435 | TGTCTCTTGCTTAGAGTGTGTAAATCAAGGAGCCATCATTAATGTTTATTT | 1494 | PR | 18-SEP-1998; | 98US-0100848P; |
| | | | | PR | 18-SEP-1998; | 98US-0100849P; |
| Db | 1464 | TGTCTCTTGCTTAGAGTGTGTAAATCAAGGAGCCATCATTAATGTTTATTT | 1523 | PR | 18-SEP-1998; | 98US-0101014P; |
| | | | | PR | 18-SEP-1998; | 98US-0101068P; |
| QY | 1495 | CTCTC 1499 | | PR | 22-SEP-1998; | 98US-0101071P; |
| | | | | PR | 22-SEP-1998; | 98US-0101279P; |
| Db | 1524 | CTCTC 1528 | | PR | 23-SEP-1998; | 98US-0101471P; |
| | | | | PR | 23-SEP-1998; | 98US-0101472P; |
| RESULT 9 | | | | | | |
| AAA37041 | | | | | | |
| ID | AAA37041 | standard; cDNA; 1564 BP. | | | | |
| AC | AAA37041; | | | | | |
| XX | | | | | | |
| DT | 08-AUG-2000 | (first entry) | | | | |
| DE | Human PR01248 | (UNQ631) cDNA sequence SEQ ID NO:67. | | | | |
| KW | Human; PRO polypeptide; membrane bound protein; receptor; diagnosis; | | | | | |
| KW | transmembrane; secretion; immunocathesion; pharmaceutical; screening; ss. | | | | | |
| OS | Homo sapiens. | | | | | |
| PN | W0200012708-A2. | | | | | |
| XX | | | | | | |
| PD | 09-MAR-2000. | | | | | |
| PF | | | | | | |
| XX | 01-SEP-1999; | 99WO-US020111. | | | | |
| PR | 01-SEP-1998; | 98US-0098716P. | | | | |
| PR | 01-SEP-1998; | 98US-0098749P. | | | | |
| PR | 01-SEP-1998; | 98US-0098750P. | | | | |
| PR | 02-SEP-1998; | 98US-0098803P. | | | | |
| PR | 02-SEP-1998; | 98US-0098821P. | | | | |
| PR | 02-SEP-1998; | 98US-0098843P. | | | | |
| PR | 09-SEP-1998; | 98US-0099530P. | | | | |
| PR | 09-SEP-1998; | 98US-0099596P. | | | | |
| PR | 09-SEP-1998; | 98US-0099598P. | | | | |
| PR | 09-SEP-1998; | 98US-0099602P. | | | | |
| PR | 09-SEP-1998; | 98US-0099642P. | | | | |
| PR | 10-SEP-1998; | 98US-0099741P. | | | | |
| PR | 10-SEP-1998; | 98US-0099753P. | | | | |
| PR | 10-SEP-1998; | 98US-0099763P. | | | | |
| PR | 10-SEP-1998; | 98US-0099792P. | | | | |
| PR | 10-SEP-1998; | 98US-0099808P. | | | | |
| PR | 10-SEP-1998; | 98US-0099812P. | | | | |
| PR | 10-SEP-1998; | 98US-0099815P. | | | | |
| PR | 10-SEP-1998; | 98US-0099816P. | | | | |
| PR | 15-SEP-1998; | 98US-0100308P. | | | | |
| PR | 15-SEP-1998; | 98US-0100388P. | | | | |
| PR | 15-SEP-1998; | 98US-0100390P. | | | | |
| PR | 16-SEP-1998; | 98US-0100584P. | | | | |
| PR | 16-SEP-1998; | 98US-0100627P. | | | | |
| PR | 16-SEP-1998; | 98US-0100661P. | | | | |
| PR | 16-SEP-1998; | 98US-0100662P. | | | | |

Db 1044 CTGGGTCTTCAGGAATCAGTGTCTGGAGGAAAGATGGCCAGCAATTCAGCATGTGT 1103
Qy 1040 CTTTCTGCAAGTGTCTTATCACACCTCCCTCCAGCCCAACGCGCTCAGCCCGAGCC 1099
Db 1104 CTTTCTGCAAGTGTCTTATCACACCTCCCTCCAGCCCAACGCGCTCAGCCCGAGCC 1163
Qy 1100 CCAGCTCAGCCCTGAGGACAGCTCTGATGGGAGAGTGGGCCCCCTGAGCCCACTGGGT 1159
Db 1164 CCAGCTCAGCCCTGAGGACAGCTCTGATGGGAGAGTGGGCCCCCTGAGCCCACTGGGT 1223
Qy 1160 CTTGAGGCTGCACTGGAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1219
Db 1224 CTTGAGGCTGCACTGGAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1283
Qy 1220 TGGAGTGCCCATGCACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1279
Db 1284 TGGAGTGCCCATGCACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1343
Qy 1280 GTCCCTCTCTCCCAAGTGTCCACAGTCACTGAGCCAGAGGTGGTGGAAACATGAGAC 1339
Db 1344 GTCCCTCTCTCCCAAGTGTCCACAGTCACTGAGCCAGAGGTGGTGGAAACATGAGAC 1403
Qy 1340 TCGAGGCTGAGGCTGATCTGAACACACAGCCCTGTACTTGGGTTGGCTCTGTGTGTGT 1399
Db 1404 TCGAGGCTGAGGCTGATCTGAACACACAGCCCTGTACTTGGGTTGGCTCTGTGTGTGT 1463
Qy 1400 GAACTCTGTGTACCAAGTGTGAGAGAAATTTGTCTCTGTGTGTGTGTGTGTGTGTGT 1459
Db 1464 GAACTCTGTGTACCAAGTGTGAGAGAAATTTGTCTCTGTGTGTGTGTGTGTGTGTGT 1523
Qy 1460 TAAATCAAGGAAGCCATTAATTTGTTTATTTCTCTC 1499
Db 1524 TAAATCAAGGAAGCCATTAATTTGTTTATTTCTCTC 1563

RESULT 10

AAF54249
ID AAF54249 standard; DNA; 1564 BP.
XX
AC AAF54249;
DX 02-APR-2001 (first entry)
XX
DE DNA encoding protein of the invention #20.
XX
KW Secreted; transmembrane; gene therapy; ss.
XX
OS Unidentified.
XX
PN WO200078961-A1.
XX
PD 28-DEC-2000.
XX
PF 18-FEB-2000; 2000WO-US004342.
XX
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.

PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000316.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart FA, Tumas D, Watanabe CK;
PI Williams PM, Wood W;
XX
WI WPI; 2001-071395/08.
XX
PT Secreted and transmembrane proteins and nucleic acids designated PRO,
PT useful as hybridization probes, in chromosome and gene mapping and gene
PT therapy.
XX
PS Claim 2; Fig 39; 787pp; English.
XX
CC The present invention relates to secreted and transmembrane proteins.
CC These proteins and the DNA encoding them may be used as hybridization
CC probes, in chromosome and gene mapping and in the generation of anti-
CC sense RNA and DNA. They may also be used to generate either
CC transgenic animals or knockout animals which are in turn useful for
CC development and screening of therapeutically useful reagents. The nucleic
CC acids may also be used in gene therapy
XX
SQ Sequence 1564 BP; 314 A; 430 C; 441 G; 379 T; 0 U; 0 Other;

Query Match 98.3%; Score 1473.6; DB 4; Length 1564;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1476; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 20 AGGTGTGGGCTTTCTGGCCAGCAAGCTGATGAAGCTCTTATCTTGTGTG 79
Db 84 AGGTGTGGGCTTTCTGGCCAGCAAGCTGATGAAGCTCTTATCTTGTGTG 143
Qy 80 CCGTGTGGGCTTTCTGGCCAGCTGAGCCACAGAGTTCTGAGATATCC 139
Db 144 CTGTGTGGGCTTTCTGGCCAGCTGAGCCACAGAGTTCTGAGATATCC 203
Qy 140 GGTGCAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCATATTACACCAAGATG 199
Db 204 GGTGCAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCATATTACACCAAGATG 263
Qy 200 TATCCAGAGGACTGCAACTGCTGCAGTGTGGAGCCCATGCCAGTGGCTGGCCATG 259
Db 264 TATCCAGAGGACTGCAACTGCTGCAGTGTGGAGCCCATGCCAGTGGCTGGCCATG 323
Qy 260 AGTGGAGGCTACTGCTGTGGAGTSCAGTACGAGGAGCGACACACCA 319
Db 324 AGTGGAGGCTACTGCTGTGGAGTSCAGTACGAGGAGCGACACACCA 383
Qy 320 TCAAGTCAATCTTGTCTTACCTGTCCGTGGTGGTGGCTGTCTCTACATGGCT 379
Db 384 TCAAGTCAATCTTGTCTTACCTGTCCGTGGTGGTGGCTGTCTCTACATGGCT 443
Qy 380 TCGTGTGTGGAGCCCTCTGATCCGAAAGCGGATGATACACTGAGGACTGACCA 439
Db 444 TCGTGTGTGGAGCCCTCTGATCCGAAAGCGGATGATACACTGAGGACTGACCA 503
Qy 440 ATGAGGAGGAGATGAGGATGCTGCTCTATGGCAGCAGCTGCTGATCCCTGGGAGAC 499

Db 504 ATGAGGAGGAGATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCAATCCCTCGGGGGAC 563
Qy 500 CCCAGCAAAACACAGTCTCTGAGCGGTGTGAAAGGTGCCAGCAGGGGTGGAAGCTGCAAG 559
Db 564 CCGAGCAAAACACAGTCTCTGAGCGGTGTGAAAGGTGCCAGCAGGGGTGGAAGCTGCAAG 623
Qy 560 TCGAGGAGGAGGAGGAGAGAGTCTTTCGATCGGCAAGATGCTCAGCTAGATGGGCTGGT 619
Db 624 TCGAGGAGGAGGAGGAGAGAGTCTTTCGATCGGCAAGATGCTCAGCTAGATGGGCTGGT 683
Qy 620 TGGGTTGGGTCAGAGGCCCAACACCATGGCTGCCAGCTTCCAGGCTGACAAAGCAGGGG 679
Db 684 GTGGTTGGGTCAGAGGCCCAACACCATGGCTGCCAGCTTCCAGGCTGACAAAGCAGGGG 743
Qy 680 GCTACTTCTCCCTCCCTGGGTTCAGAGTCTTCCCTTTAAAGCCTGTGGCAATTTTCTC 739
Db 744 GCTACTTCTCCCTCCCTGGGTTCAGAGTCTTCCCTTTAAAGCCTGTGGCAATTTTCTC 803
Qy 740 CTTCTCCCTACTTTAGAAATGTTGACTTGGCTATTTGATTAGGAGAGAGGATGG 799
Db 804 CTTCTCCCTACTTTAGAAATGTTGACTTGGCTATTTGATTAGGAGAGAGGATGG 863
Qy 800 TCTCTGATCTCTGTTCTTCTTGGGTCTTTGGGTTGAAGGATGGGAAAGCAGGCCA 859
Db 864 TCTCTGATCTCTGTTCTTCTTGGGTCTTTGGGTTGAAGGATGGGAAAGCAGGCCA 923
Qy 860 GAAGGAGATGAGACATTCGAGAGGGGCTCAGAGTGGATGGATCTGTCTCTCTGGCT 919
Db 924 GAAGGAGATGAGACATTCGAGAGGGGCTCAGAGTGGATGGATCTGTCTCTCTGGCT 983
Qy 920 CCACTTCTGGCGCTTCAGAGTCTGAGTCTTGGGAATGTTTACCCCTGGAAGATAAAG 979
Db 984 CCACTTCTGGCGCTTCAGAGTCTGAGTCTTGGGAATGTTTACCCCTGGAAGATAAAG 1043
Qy 980 CTGGGTTCTCAGGAATCAGTCTCTGGGAGGAAAGCATGGCCAGCATTCAGCATGTGT 1039
Db 1044 CTGGGTTCTCAGGAATCAGTCTCTGGGAGGAAAGCATGGCCAGCATTCAGCATGTGT 1103
Qy 1040 CTTTCTGCACTGGTCTTATCACACCTCCCTCCAGCCCAAGGGCTCAGGCCCAGCC 1099
Db 1104 CTTTCTGCACTGGTCTTATCACACCTCCCTCCAGCCCAAGGGCTCAGGCCCAGCC 1163
Qy 1100 CCAAGCTCCAGCCCTGAGGACAGCTCTGATGGGAGAGCTGGGCGCCCTGAGCCCACTGGGT 1159
Db 1164 CCAAGCTCCAGCCCTGAGGACAGCTCTGATGGGAGAGCTGGGCGCCCTGAGCCCACTGGGT 1223
Qy 1160 CTTCAGGTTGCACTGGAAGTGGTGTCTGCTGTCCCTGTGCACTTCTCCACTGGGGCA 1219
Db 1224 CTTCAGGTTGCACTGGAAGTGGTGTCTGCTGTCCCTGTGCACTTCTCCACTGGGGCA 1283
Qy 1220 TGGAGTGGCAATGCATCTCTGCTGCCGCTCCCTCAGCTGCACTTGAAGGCTCTGGCA 1279
Db 1284 TGGAGTGGCAATGCATCTCTGCTGCCGCTCCCTCAGCTGCACTTGAAGGCTCTGGCA 1343
Qy 1280 GTCCTCTCTCCCAAGTCTCCAGTCACTGAGCCAGAGGCTCGGTTGGAACATGAGAC 1339
Db 1344 GTCCTCTCTCCCAAGTCTCCAGTCACTGAGCCAGAGGCTCGGTTGGAACATGAGAC 1403
Qy 1340 TCGAGGCTGAGCGTGAATCGAACACACAGCCCTGTACTTGGGTTGCCCTCTTGTCCCT 1399
Db 1404 TCGAGGCTGAGCGTGAATCGAACACACAGCCCTGTACTTGGGTTGCCCTCTTGTCCCT 1463
Qy 1400 GAACITCTGTTGTACCAAGTGCATGGAGAGAAAATTTTGTCTCTTCTTAGAGTTGTGTG 1459

Db 1464 GAACITCTGTTGTACCAAGTGCATGGAGAGAAAATTTTGTCTCTTCTTAGAGTTGTGTG 1523
Qy 1460 TAAATCAAGAGGCCATCAATAAATGTTTAAATTTTAAATTTCTCTC 1499
Db 1524 TAAATCAAGAGGCCATCAATAAATGTTTAAATTTTAAATTTCTCTC 1563
RESULT 11
AAS46047
ID AAS46047 standard; cDNA; 1564 BP.
XX AAS46047;
AC AAS46047;
XX 18-DEC-2001 (first entry)
DE Human DNA encoding PRO polypeptide sequence #123.
XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW PCR primer.
XX Homo sapiens.
XX WO200168848-A2.
XX 20-SEP-2001.
XX 28-FEB-2001; 2001WO-US006520.
XX 01-MAR-2000; 2000WO-US005601.
XX 02-MAR-2000; 2000WO-US005841.
XX 03-MAR-2000; 2000US-0187202P.
XX 06-MAR-2000; 2000US-0186968P.
XX 14-MAR-2000; 2000US-0189320P.
XX 14-MAR-2000; 2000US-0189328P.
XX 15-MAR-2000; 2000WO-US006884.
XX 21-MAR-2000; 2000US-0190528P.
XX 21-MAR-2000; 2000US-0191007P.
XX 21-MAR-2000; 2000US-0191048P.
XX 21-MAR-2000; 2000US-0191314P.
XX 28-MAR-2000; 2000US-0192655P.
XX 29-MAR-2000; 2000US-0193032P.
XX 29-MAR-2000; 2000US-0193053P.
XX 30-MAR-2000; 2000WO-US006849.
XX 04-APR-2000; 2000US-0194449P.
XX 04-APR-2000; 2000US-0194647P.
XX 11-APR-2000; 2000US-0195975P.
XX 11-APR-2000; 2000US-0196000P.
XX 11-APR-2000; 2000US-0196187P.
XX 11-APR-2000; 2000US-0196690P.
XX 11-APR-2000; 2000US-0196820P.
XX 18-APR-2000; 2000US-0198121P.
XX 18-APR-2000; 2000US-0198585P.
XX 25-APR-2000; 2000US-0198977P.
XX 25-APR-2000; 2000US-0199550P.
XX 25-APR-2000; 2000US-0199654P.
XX 03-MAY-2000; 2000US-0201516P.
XX 17-MAY-2000; 2000WO-US013705.
XX 22-MAY-2000; 2000WO-US014042.
XX 30-MAY-2000; 2000WO-US014941.

PR 02-JUN-2000; 2000WO-US015264.
 PR 03-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000WO-US034956.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 XX P-PSDB; AAU29146.
 DR WPI; 2001-602746/68.
 XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 PT presence of tumors, such as prostate and breast tumors, in mammals and to
 PT screen for modulators of the compounds.
 XX Claim 2; Fig 245; 774pp; English.
 CC Sequences AA545925-AA546231 represent DNA molecules encoding and PCR
 CC primers for PRO polypeptides of the invention. The sequences of the
 CC invention can be used to detect the presence of a tumour in a mammal by
 CC comparing the level of expression of a PRO polypeptide in a test sample
 CC of cells from the animal and a control sample of normal cells, whereby a
 CC higher level of expression in the test sample indicates the presence of a
 CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
 CC pigs, goats and rabbits but are preferably human. The polypeptides can be
 CC used to stimulate tumour necrosis factor (TNF) alpha release from human
 CC blood, when contacted with it. A specific polypeptide can be used to
 CC stimulate the proliferation or differentiation of chondrocyte cells. The
 CC PRO proteins can be used to determine the presence of tumours and also
 CC susceptibility to tumour development, particularly adrenal, lung, colon,
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders
 XX
 SQ Sequence 1564 BP; 314 A; 430 C; 441 G; 379 T; 0 U; 0 Other;
 Query Match 98.3%; Score 1473.6; DB 4; Length 1564;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1476; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 20 AGGTGTCCGGCTTTGCTGGCCACGAAAGCCTGATAAAGCATGAAGCTCTTATCTTTGGTGG 79
 DB 84 AGGTGTCCGGCTTTGCTGGCCACGAAAGCCTGATAAAGCATGAAGCTCTTATCTTTGGTGG 143
 QY 80 CGGTGTGGGGTGTGCTGGTGGCCCGCCAGCTGAAGCCACACAGAGTTCGAAGATATCC 139
 DB 144 CTGTGTGGGTGTGCTGGTGGTGGCCCGCCAGCTGAAGCCACACAGAGTTCGAAGATATCC 203
 QY 140 GGTGCAATGCACTCTGCAACCTTATAGAAACATCAGTGGGCAATTTACACACAGATG 199
 DB 204 GGTGCAATGCACTCTGCAACCTTATAGAAACATCAGTGGGCAATTTACACACAGATG 263
 QY 200 TATCCACAGAAAGACTGCAATGCTGCTGCACTGGTGGAGCCCATGCACTGGTGGCATG 259
 DB 264 TATCCACAGAAAGACTGCAATGCTGCTGCACTGGTGGAGCCCATGCACTGGTGGCATG 323
 QY 260 ACGTGGAGGCTACTGCTGCTGTGGAGTGTGAGGTACGAGGAGGCGCAGCACCAACCA 319

DB 324 ACGTGGAGGCTACTGCTGCTGTGCGAGTGCAGGTACGAGGAGGCGCAGCACCAACCA 383
 QY 320 TCAAGTCAATCAATTCATCACTGTCCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 379
 DB 384 TCAAGTCAATCAATTCATCACTGTCCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 443
 QY 380 TCGTGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 439
 DB 444 TCGTGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 503
 QY 440 ATCAGGAGGAGATGAGGATGCTGCTCTATGGCAGCAGCTGCTGCATCCCTCGGGGGAC 499
 DB 504 ATCAGGAGGAGATGAGGATGCTGCTCTATGGCAGCAGCTGCTGCATCCCTCGGGGGAC 563
 QY 500 CCGGAGCAAAACAAGTCTCTGGAGGCTGTGGAAGGTGCCAGCAGCGGTGGAAGCTGCAAG 559
 DB 564 CCGGAGCAAAACAAGTCTCTGGAGGCTGTGGAAGGTGCCAGCAGCGGTGGAAGCTGCAAG 623
 QY 560 TCGAGGAGCAGCGGAGAGACAGTCTCTGATCGGCGCAAGATGCTCAGCTAGATGGGCTGGT 619
 DB 624 TCGAGGAGCAGCGGAGAGACAGTCTCTGATCGGCGCAAGATGCTCAGCTAGATGGGCTGGT 683
 QY 620 GTGGTGGGTCAAGGCCCCAACACATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGG 679
 DB 684 GTGGTGGGTCAAGGCCCCAACACATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGG 743
 QY 680 GTTACTTCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTT 739
 DB 744 GTTACTTCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTT 803
 QY 740 GTTCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTT 799
 DB 804 GTTCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTT 863
 QY 800 TCTCTGATCTCTGTCT 859
 DB 864 TCTCTGATCTCTGTCT 923
 QY 860 GAAAGGAATGGAGACATTCGAGGCGGCTCAGGAGTGGATGGATGCTCTCTCTCTCTCTCTCT 919
 DB 924 GAAAGGAATGGAGACATTCGAGGCGGCTCAGGAGTGGATGGATGCTCTCTCTCTCTCTCTCT 983
 QY 920 CCACTCTTGGCGCTTCCAGGCTCTGAGTCTTGGGATGTGTACCTTGGAGATTAAG 979
 DB 984 CCACTCTTGGCGCTTCCAGGCTCTGAGTCTTGGGATGTGTACCTTGGAGATTAAG 1043
 QY 980 CTGGGTCTTCAAGAACTCAGTGTCTGGAGGAAAGCATGGCCAGCATTCAGCATGTCT 1039
 DB 1044 CTGGGTCTTCAAGAACTCAGTGTCTGGAGGAAAGCATGGCCAGCATTCAGCATGTCT 1103
 QY 1040 CTTTCTGCACTGGTCTTATCAGCACCTCCCTCCAGGCCCCAGGCGCTCAGCCCCAGCC 1099
 DB 1104 CTTTCTGCACTGGTCTTATCAGCACCTCCCTCCAGGCCCCAGGCGCTCAGCCCCAGCC 1163
 QY 1100 CCAAGTCCAGCCCTGAGGAGCAGCTCTGATGGGAGCTGGGCGCCCTGAGCCCATGGGT 1159
 DB 1164 CCAAGTCCAGCCCTGAGGAGCAGCTCTGATGGGAGCTGGGCGCCCTGAGCCCATGGGT 1223
 QY 1160 CTTTCAAGGAGTCACTGGAGCTGGTGTCTGCTCTCCCTGTGCACTCTCTGCACTGGGCA 1219
 DB 1224 CTTTCAAGGAGTCACTGGAGCTGGTGTCTGCTCTCCCTGTGCACTCTCTGCACTGGGCA 1283

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|-----------|---|---|------|
| QY | 1220 | TGAGGTGGCCAGTGCATCTCTGCTGCTGCCGGTCCCTCCTCCTGCACTTAGAGGGGTCTGGGGCA | 1279 |
| DB | 1284 | TGAGGTGGCCAGTGCATCTCTGCTGCTGCCGGTCCCTCCTCCTGCACTTAGAGGGGTCTGGGGCA | 1343 |
| QY | 1280 | GTCCCTGCTCTCCCCAGTGTCCACATCAGCTGAGGCCAGAGGGTGGTGGAAATCATGAGAC | 1339 |
| DB | 1344 | GTCCCTGCTCTCCCCAGTGTCCACATCAGCTGAGGCCAGAGGGTGGTGGAAATCATGAGAC | 1403 |
| QY | 1340 | TGGAGGCTGAGCGTGGATCTGAACACACAGCCCTGTACTTGGGTTGCCTCTTGTCCCT | 1399 |
| DB | 1404 | TGGAGGCTGAGCGTGGATCTGAACACACAGCCCTGTACTTGGGTTGCCTCTTGTCCCT | 1463 |
| QY | 1400 | GAATCTGCTGTACACAGTGCATGGAGAGAAAATTTGTCCTCTTGTCTTAGAGTTGTGTG | 1459 |
| DB | 1464 | GAATCTGCTGTACACAGTGCATGGAGAGAAAATTTGTCCTCTTGTCTTAGAGTTGTGTG | 1523 |
| QY | 1460 | TAAATCAAGGAGGCATCATTTAAATTTGTTTATTTCTCTC | 1499 |
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| RESULT 12 | | | |
| ABX78650 | | | |
| ID | ABX78650 standard; cDNA; 1564 BP. | | |
| XX | ABX78650; | | |
| XX | 15-APR-2003 (first entry) | | |
| DT | Human PRO polynucleotide #123. | | |
| DE | Human; PRO; gene; ss; cytotstatic; tumour; cancer; breast; lung; stomach; | | |
| KW | liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT; | | |
| KW | antibody-dependent enzyme mediated produg therapy. | | |
| OS | Homo sapiens. | | |
| XX | US2003027272-A1. | | |
| PN | 06-FEB-2003. | | |
| PD | 21-JUN-2002; 2002US-00176492. | | |
| PF | 18-SEP-1997; 97US-0059263P. | | |
| XX | 18-SEP-1997; 97US-0059266P. | | |
| PR | 17-OCT-1997; 97US-0062250P. | | |
| PR | 21-OCT-1997; 97US-0063486P. | | |
| PR | 24-OCT-1997; 97US-0063120P. | | |
| PR | 28-OCT-1997; 97US-0063121P. | | |
| PR | 28-OCT-1997; 97US-0063540P. | | |
| PR | 28-OCT-1997; 97US-0063541P. | | |
| PR | 28-OCT-1997; 97US-0063544P. | | |
| PR | 28-OCT-1997; 97US-0063564P. | | |
| PR | 29-OCT-1997; 97US-0063734P. | | |
| PR | 31-OCT-1997; 97US-0063870P. | | |
| PR | 31-OCT-1997; 97US-0064103P. | | |
| PR | 13-NOV-1997; 97US-0065311P. | | |
| PR | 21-NOV-1997; 97US-0066120P. | | |
| PR | 24-NOV-1997; 97US-0066466P. | | |
| PR | 24-NOV-1997; 97US-0066772P. | | |
| PR | 11-DEC-1997; 97US-0069333P. | | |
| PR | 12-DEC-1997; 97US-0069425P. | | |
| PR | 17-DEC-1997; 97US-0069870P. | | |

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| PR | 12-JUN-1995; | 98US-00891035P; |
| PR | 16-JUN-1995; | 98US-00895121P; |
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| PR | 22-JUN-1995; | 98US-00902462P; |
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| PR | 26-JUN-1995; | 98US-00103413P; |
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| PR | 26-JUN-1995; | 98US-00908663P; |
| PR | 26-JUN-1995; | 98US-00910101P; |
| PR | 01-JUL-1995; | 98US-00913595P; |
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| PR | 02-JUL-1995; | 98US-00914769P; |
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| PR | 02-JUL-1995; | 98US-00916268P; |
| PR | 02-JUL-1995; | 98US-00916269P; |
| PR | 02-JUL-1995; | 98US-00916326P; |
| PR | 02-JUL-1995; | 98US-00916328P; |
| PR | 24-JUL-1995; | 98US-00940068P; |
| PR | 24-AUG-1995; | 98US-00952822P; |
| PR | 17-AUG-1995; | 98US-00959598P; |
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| PR | 18-AUG-1995; | 98US-00963649P; |
| PR | 17-AUG-1995; | 98US-00963959P; |
| PR | 17-AUG-1995; | 98US-00967576P; |
| PR | 17-AUG-1995; | 98US-00967667P; |
| PR | 17-AUG-1995; | 98US-00968675P; |
| PR | 17-AUG-1995; | 98US-00969911P; |
| PR | 17-AUG-1995; | 98US-00969979P; |
| PR | 26-AUG-1995; | 98US-00973546P; |
| PR | 26-AUG-1995; | 98US-00973555P; |
| PR | 26-AUG-1995; | 98US-00973711P; |
| PR | 26-AUG-1995; | 98US-00973747P; |
| PR | 26-AUG-1995; | 98US-00980141P; |
| PR | 01-SEP-1995; | 98US-00980146P; |
| PR | 01-SEP-1995; | 98US-00987232P; |
| PR | 01-SEP-1995; | 98US-00988033P; |
| PR | 02-SEP-1995; | 98US-00988211P; |
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| PR | 10-SEP-1995; | 98US-00997545P; |
| PR | 10-SEP-1995; | 98US-00997633P; |
| PR | 10-SEP-1995; | 98US-00998122P; |
| PR | 10-SEP-1995; | 98US-00998123P; |

Query Match 98.38; Score 1473.6; DB 7; Length 1564;

Best Local Similarity 99.7%; Pred. No. 0;

2008 Year Summary 05/10/07 11:00 AM
Matches 1476; Conservative 0; Mismatches 0

Matches 1476; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

20 AGGTGTCGGCTTTGCTGGCCAGCAAGCCTGATAAGCATGAAGCTCTTATCTTGGTGG 79

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Z0 AAGG19100000C:1100C1000000CAACCC10A1AA00ATGATACC101TATC11139109 / 75

64 AGGTGTCGGGCTTTGCTGGCCAGCAAGCCTGATAAGCATGAAGCTCTTATCTTTGGTGG 143

54 AGGTGTCTCCGCTTTGCTGGCCCAAGCCCTGATATAGCATGATAGCTCTATCTTTGGTGGTATG

80 CCGTGGTCGGGGTGTGTGCTGGTGGCCCGCAGCCACACAGAGCTTCTGAAGATATCC 139

50 CCCTGGTGGGTGTTGGCTGGTGGCTCCAGCTGATAGCCGACACATAGAGTCTCTGAGAGATATCC 135

144 CTTGGTGGGGTCTTTCCTGGTGGCCCAAGCTGAAGCCACAGCACTTGAATATCC

144 C.TGTTGGTCTTGCTGGTGCCTCCCAAGCAGAAGAGATTCGACAGATAATCC 203

140 GGTGCAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCATATTTACACCGAATG 199

140 GGCGCAATGCAICIGGCCAATATAGATAACATCAGTGGCAATATTACATCCAGAAATG 199

[illegible]

204 GGTGCAAAAGCATCTGTCCACCTTATAGAAACATCAGTGGCA.CATT.TA.CAACCGAATG 263

[illegible]

200 TATCCCAAGGAACTGCAACTGCCCTGCACCTGGTGGAGCCCATGCCAGTGCCTGGCCATG 259

251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 1115 1116 1117 1118 1119 1120 1121 1122 1123 1124 1125 1126 1127 1128 1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145 1146 1147 1148 1149 1150 1151 1152 1153 1154 1155 1156 1157 1158 1159 1160 1161 1162 1163 1164 1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183 1184 1185 1186 1187 1188 1189 1190 1191 1192 1193 1194 1195 1196 1197 1198 1199 1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 121

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260 ACGTGGAGGCCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAGCACCAACCA 319

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324 ACGTGGAGGCCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGGCGACGACCA 383

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320 TCAAGTCATCATTTGTCACTACCTGTCCGTGGTGGTGCCCTGTTGCTCTACATGGCCT 379

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QY 380 TCTTGATGCTGGTGAAGCCCTCTGATCCGAAAGCCGGATGCGATCACTGAGCAACTGCACA 439
 Db 444 TCTTGATGCTGGTGAAGCCCTCTGATCCGAAAGCCGGATGCGATCACTGAGCAACTGCACA 503
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 QY 500 CCGGAGCAACACAGTCTGAGCCTGTGGAGGTGCCAGCAGCCGCTGGAAGCTGCAGG 559
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 QY 560 TCGAGGAGCGGAGAGACAGTCTTCGATCGGCAAGATGCTCAGCTAGATGGCTGCT 619
 Db 624 TCGAGGAGCGGAGAGACAGTCTTCGATCGGCAAGATGCTCAGCTAGATGGCTGCT 683
 QY 620 GTGGTGGGTCAAGGCCCCAACACACATGGCTGCCAGCTCCAGGCTGGAAGAGAGGG 679
 Db 684 GTGGTGGGTCAAGGCCCCAACACACATGGCTGCCAGCTCCAGGCTGGAAGAGAGGG 743
 QY 680 GCTACTTCCCTTCCCTCCGCTCCAGCTCTTCCCTTTAAAGGCTGTGGCATTTTCTCTC 739
 Db 744 GCTACTTCCCTTCCCTCCGCTCCAGCTCTTCCCTTTAAAGGCTGTGGCATTTTCTCTC 803
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 QY 800 TCTCTGATCTCTGTCTCTCTCTGGGTCTTTGGGCTTGAAGGATGGGAGAGAGAGGCA 859
 Db 864 TCTCTGATCTCTGTCTCTCTCTGGGTCTTTGGGCTTGAAGGATGGGAGAGAGAGGCA 923
 QY 960 GAAAGGAAATGAGAGCAATCAGAGCGGCTCAGAGTGGATGGATCTGTCTCTCTGGCT 919
 Db 924 GAAAGGAAATGAGAGCAATCAGAGCGGCTCAGAGTGGATGGATCTGTCTCTCTGGCT 983
 QY 920 CCACTCTTCCGCGCTTCCAGCTCTGAGTCTTGGGAGTGTATACCTTCGAGAGATAAG 979
 Db 984 CCACTCTTCCGCGCTTCCAGCTCTGAGTCTTGGGAGTGTATACCTTCGAGAGATAAG 1043
 QY 980 CTGGGTCTTCAGGAACTCAGTGTCTGGAGAGAAAGCATGGCCAGCATTCAGCATGTCT 1039
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 Db 1224 CTTTCAAGGTGCACTGGAAGCTGGTGTTCGCTGTCCCTGTGCACTTCTGCACTGGGGA 1283
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 Db 1284 TGAAGTGCCATGCACTCTGCTGCGGTCCCTTACCTTCACTTCACTTGAAGGCTGGGCA 1343
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 Db 1344 GTCCCTCTCTCCCACTGTCCCACTCACTGAGCCAGAGGCTCGGTTGGAACATGAGAC 1403

QY 1340 TCGAGGCTGAGGCTGGATCTGAAACACACAGCCCTGTACTTGGGTGGCTCTGTGCTT 1399
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 QY 1400 GAACTTCGTTGTACAGTGCATGGAGAGAAAATTTTGTCTTGTCTTAGAGTTGTG 1459
 Db 1464 GAACTTCGTTGTACAGTGCATGGAGAGAAAATTTTGTCTTGTCTTAGAGTTGTG 1523
 QY 1460 TAAATCAAGAGAGCCATCATTAAATTTTATTCTCTC 1499
 Db 1524 TAAATCAAGAGAGCCATCATTAAATTTTATTCTCTC 1563

RESULT 13
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 ID ACA75622 standard; cDNA; 1564 BP.
 AC
 XX ACA75622;
 XX
 D7 07-JUL-2003 (first entry)
 DE
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 XX
 XX Novel human secreted and transmembrane protein: PRO1248 cDNA.
 KW Human; secreted and transmembrane protein: PRO; gene therapy;
 KW tumour necrosis factor-alpha release; TNF-alpha release;
 KW chondrocyte proliferation; chondrocyte differentiation; tumour;
 KW adrenal tumour; lung tumour; colon tumour; breast tumour;
 KW prostate tumour; rectal tumour; cervical tumour; liver tumour; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2003032127-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 26-JUN-2002; 2002JUS-00183012.
 XX
 PR 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059266P.
 PR 17-OCT-1997; 97US-0062250P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 28-OCT-1997; 97US-0063540P.
 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 21-NOV-1997; 97US-0066120P.
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Qy 260 AGGTGAGGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 319
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Db 564 CCGAGCAAAACACATCTCTGGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 623
Qy 560 TSCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 619

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| XX | |
| XX | ACC87630; |
| XX | |
| DT | 05-AUG-2003 (first entry) |
| XX | |
| XX | |
| DE | Human secreted polypeptide PRO1248-encoding cDNA, SEQ ID NO:245. |
| XX | |
| KW | Human; PRO; secreted protein; transmembrane protein; |
| KW | extracellular domain; tumour necrosis factor-alpha; TNF-alpha; |
| KW | chondrocyte; proliferation; differentiation; cartilage disorder; |
| KW | bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; |
| KW | adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; |
| KW | liver; drug screening; transgenic animal; genetic analysis; |
| KW | antiarthritic; vulnuary; gene therapy; gene; ss. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| US | US2003027278-A1. |
| XX | |
| PD | 06-FEB-2003. |
| XX | |
| PF | 21-JUN-2002; 2002US-0017697F. |
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Y 80 CCGTGTGGGTGTTTGGTGGTGGCCAGCAGCCTGATAGCATGAGCTCTATCTTTGGTG 139
D 144 CTGTGGTGGGTGTTTGGTGGTGGCCAGCAGCCTGATAGCATGAGCTCTATCTTTGGTG 203
Y 140 GGTGCAATGCACTCTGCACTCTATAGCAATGATGATGATGATGATGATGATGATG 199
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D 264 TATCCAGAGGACTGCACTGCTGCACTGCTGCACTGCTGCACTGCTGCACTGCTG 323
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D 864 TCTCTGATCTCTGTTGTTCTTCTTGGGTCTTTGGGTGTTAGGGAGGAGGAGGAGGAG 923
Y 860 GAAGGAGATGAGACATTCAGAGGCGGCTCAGAGGATGGATGGATCTGCTCTCTGGCT 919
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D 984 CCACTCTTGGCGCTTCCAGCTCTGAGTCTTGGGATGTTTACCTTGGAAATTAAG 1043
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Y 1100 CCACTCTCCAGGCTTGAAGAGCTCTGATGGGAGAGCTGGGCGGCTCAGGCGGAGGCG 1159
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Y 1160 CTTTGGGTGCACTGGAAGCTGGTGTGCTGTCCCTGTGGCTTCTGGCACTTCTGGCACT 1219
D 1224 CTTTGGGTGCACTGGAAGCTGGTGTGCTGTCCCTGTGGCTTCTGGCACTTCTGGCACT 1283
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D 1284 TGGAGTGCCCATGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1343
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Search completed: April 3, 2004, 03:01:48
Job time : 361.536 secs

Run on: April 3, 2004, 11:14:53 ; Search time 360.216 Seconds
(without alignments)
15564.412 Million cell updates/sec

REFLECT score: 1499
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Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 4932372

Maximum DB seq length: 200000000

Maximum Match 100%
Listing first 45 summaries

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16: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:
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For more information, contact the publisher at 1-800-354-9700 or visit our website at www.mhprofessional.com.

and is derived by analysis of the total score distribution

| Result | Query | Score | Match | Length | DB | ID |
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| No | | | | | | |

| | | | |
|-----|--------|------|------------------|
| See | 1504 | 10 | US-09-284-320-68 |
| See | 1494.2 | 99.7 | |
| See | 1483.8 | 99.0 | US-10-153-668-95 |

| | | | | | | |
|---|------|------|------|----|--------------------|-----|
| 5 | 1480 | 98.7 | 1562 | 14 | US-10-042-211A-150 | See |
|---|------|------|------|----|--------------------|-----|

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
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| 2 | 1463.8 | 99.0 | 1519 | 14 | US-10-153-668-95 | Sequence 95, Appl |
| 3 | 1481.4 | 99.8 | 1645 | 14 | US-10-022-806-218 | Sequence 218, App |
| 4 | 1480 | 98.7 | 1562 | 14 | US-10-024-293A-150 | Sequence 150, App |
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; LENGTH: 1504

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (63)..(611)
US-09-284-320-68

Query Match 99.7%; Score 1494.2; DB 10; Length 1504;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1496; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 2

US-10-153-668-95

; Sequence 95, Application US/10153668

; Publication No. US20030092616A1

; GENERAL INFORMATION:

; APPLICANT: HONDA, Goichi

; APPLICANT: MATSUDA, Akio

; APPLICANT: MORIMATSU, Shuji

; APPLICANT: ISHIZAWA, Kenya

; TITLE OF INVENTION: STAT6 Activating Gene

; FILE REFERENCE: 1254-0207P

; CURRENT APPLICATION NUMBER: US/10/153,668

; CURRENT FILING DATE: 2002-05-24

QY 781 TTAGGGAAGAGGATGTGGTCTTGATCTGTGTGTCTTCTTGGGTCTTGGGTGAG 840
Db 786 TTAGGGAAGAGGATGTGGTCTTGATCTGTGTGTCTTCTTGGGTCTTGGGTGAG 845
QY 841 GGATGGGAGGAGGAGCCAGAAAGGATGGAGATTCAGAGCCGCTCAGAGTGGATG 900
Db 846 GAGGGGAGGAGGAGCCAGAAAGGATGGAGATTCAGAGCCGCTCAGAGTGGATG 905
QY 901 CGATCTGTCTCTCTGGCTCCACTCTTGGCCCTTCCAGCTCTGAGCTTGGGAATGTG 960
Db 906 CGATCTGTCTCTCTGGCTCCACTCTTGGCCCTTCCAGCTCTGAGCTTGGGAATGTG 965
QY 961 TTACCTTGGAGATTAAGCTGGTCTTTCAGAACTCAGTGTGSGAGAAAGCATGGC 1020
Db 966 TTACCTTGGAGATTAAGCTGGTCTTTCAGAACTCAGTGTGSGAGAAAGCATGGC 1025
QY 1021 CCAGCATTCAGATGTTTCTTCTGCAATGTTTATCACCCTTCCCTCCAGCC 1080
Db 1026 CCAGCATTCAGATGTTTCTTCTGCAATGTTTATCACCCTTCCCTCCAGCC 1085
QY 1081 CAGGCTTCAGCCAGCCAGCCAGCCAGCTCCAGCCCTGAGGACAGCTCTGATGGGAGAGCTGG 1140
Db 1086 CAGGCTTCAGCCAGCCAGCCAGCCAGCTCCAGCCCTGAGGACAGCTCTGATGGGAGAGCTGG 1145
QY 1141 CCGCTGAGCCCACTGGGTCTTCAAGGTGCACTGAGAGCTGTGTCGTGTCCCTGTG 1200
Db 1146 CCGCTGAGCCCACTGGGTCTTCAAGGTGCACTGAGAGCTGTGTCGTGTCCCTGTG 1205
QY 1201 CACTTCTGCACATGGGGCATGGAGTCCCATGATCATCTCTGCGGTGCCCTCACTG 1260
Db 1206 CACTTCTGCACATGGGGCATGGAGTCCCATGATCATCTCTGCGGTGCCCTCACTG 1265
QY 1261 CACTTGAAGGCTGTGGGCACTGCTCTCCCTCTCTCCCTGCTCCAGTGTCCAGAGTCACTGAGCCAGAG 1320
Db 1266 CACTTGAAGGCTGTGGGCACTGCTCTCCCTCTCTCCCTGCTCCAGTGTCCAGAGTCACTGAGCCAGAG 1325
QY 1321 GTCGGTTGGAACTGAGACTGAGAGGCTGAGGCTGAGTCTGAACACCAGCCCTGTACT 1380
Db 1326 GTCGGTTGGAACTGAGACTGAGAGGCTGAGGCTGAGTCTGAACACCAGCCCTGTACT 1385
QY 1381 TGGGTTGCTCTTGTCCCTGAACTTCGTTGTACAGTGCATGGAGAGAAATTTTGTCT 1440
Db 1386 TGGGTTGCTCTTGTCCCTGAACTTCGTTGTACAGTGCATGGAGAGAAATTTTGTCT 1445
QY 1441 CTGTCTTAGAGTGTGTGTAATCAAGGAAGCCATCATTAATTTTATTTCTCTC 1499
Db 1446 CTGTCTTAGAGTGTGTGTAATCAAGGAAGCCATCATTAATTTTATTTCTCTC 1504

; PRIOR APPLICATION NUMBER: US 60/293,172
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/316,031
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/328,403
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: JP 2001-157043
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: JP 2001-260681
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: JP 2001-313175
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 488
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 95
; LENGTH: 1519
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (79)..(420)
US-10-153-668-95

Query Match 99.0%; Score 1483.8; DB 14; Length 1519;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1496; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 GGGCTCTGAGGCTGTGAGGTGTCGGGCTTGTGGCCGACGAGAGCCCTGATTAAGCATG 60
DB 22 GGGCTCTGAGGCTGTGAGGTGTCGGGCTTGTGGCCGACGAGAGCCCTGATTAAGCATG 81
QY 61 AAGCTCTTATCTTTGGTGGCCGTGGTGGGTGTTGCTGGTGGCCGACGAGAGCCCTGATTAAGCATG 120
DB 82 AAGCTCTTATCTTTGGTGGCCGTGGTGGGTGTTGCTGGTGGCCGACGAGAGCCCTGATTAAGCATG 141
QY 121 AAGAGTCTGAGATATCGGTGCAAAATGCAATCTGTCCACCTTATGAACATCAAGTGGG 180
DB 142 AAGAGTCTGAGATATCGGTGCAAAATGCAATCTGTCCACCTTATGAACATCAAGTGGG 201
QY 181 CATATTACAAACAGATATGATCCAGAAAGGACTGCACTGCTGCACTGCTGCACTGCTGCACTG 240
DB 202 CATATTACAAACAGATATGATCCAGAAAGGACTGCACTGCTGCACTGCTGCACTGCTGCACTG 261
QY 241 ATGCCAGTGGCTGGCCATGAGGTGGAGGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 262 ATGCCAGTGGCTGGCCATGAGGTGGAGGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 321
QY 301 GAGGAGC 360
DB 322 GAGGAGC 381
QY 361 CTGTTGCTCTACATGGCCCTTCTGATGCTGGTGGACCCCTCTGATCCGAAAGCCGGATGCA 420
DB 382 CTGTTGCTCTACATGGCCCTTCTGATGCTGGTGGACCCCTCTGATCCGAAAGCCGGATGCA 440
QY 421 TACACTGAGCAATCTGCAATGAGGAGAGATGAGATGCTGCTCTATGCGACAGCT 480
DB 441 TACACTGAGCAATCTGCAATGAGGAGAGATGAGATGCTGCTCTATGCGACAGCT 500
QY 481 GCTGCATCCCTCGGGGGAGCCCGAGCAAAACACAGTCTGAGAGTGTGGAGGTGCCAG 540
DB 501 GCTGCATCCCTCGGGGGAGCCCGAGCAAAACACAGTCTGAGAGTGTGGAGGTGCCAG 560

QY 541 CAGCGGTGGAAGCTGCAAGTGCAGGAGCAGCGGGAAGACAGTCTTCGATCGGCAAGATG 600
DB 561 CAGCGGTGGAAGCTGCAAGTGCAGGAGCAGCGGGAAGACAGTCTTCGATCGGCAAGATG 620
QY 601 CTCAGCTAGATGGGCTGGTGTGGTCAAGGCCCAACACCATGGCTGGCGAGCTTCC 660
DB 621 CTCAGCTAGATGGGCTGGTGTGGTCAAGGCCCAACACCATGGCTGGCGAGCTTCC 680
QY 661 AGGCTGGAACAAAGCAGGGGGCTACTTCTCCCTTCCCTTCCAGTCTCCCTTAAAA 720
DB 681 AGGCTGGAACAAAGCAGGGGGCTACTTCTCCCTTCCCTTCCAGTCTCCCTTAAAA 740
QY 721 GCTGTGCAATTTTCTCCCTTCTCCCTTCTCCCTTCTCCCTTCTCCCTTCTCCCTTCTCC 780
DB 741 GCTGTGCAATTTTCTCCCTTCTCCCTTCTCCCTTCTCCCTTCTCCCTTCTCCCTTCTCC 800
QY 781 TTAGGGAAGAGGATGTGGTCTCTGATCTCTGTTGCTCTTGGGTCTTGGGGTTCAG 840
DB 801 TTAGGGAAGAGGATGTGGTCTCTGATCTCTGTTGCTCTTGGGTCTTGGGGTTCAG 860
QY 841 GGATGGGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
DB 861 GGATGGGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 920
QY 901 CGATCTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
DB 921 CGATCTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 980
QY 961 TTACCTTGGAGATTAAGCTGCTTTCAGGAACTCAGTGTCTGGGAGGAAAGCATGGC 1020
DB 981 TTACCTTGGAGATTAAGCTGCTTTCAGGAACTCAGTGTCTGGGAGGAAAGCATGGC 1040
QY 1021 CAGCATCTCAGATGTGTCTTCTGCAAGTGTCTTATCACCAGTCTCCCTCCAGGCC 1080
DB 1041 CAGCATCTCAGATGTGTCTTCTGCAAGTGTCTTATCACCAGTCTCCCTCCAGGCC 1100
QY 1081 CAGGCTCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAG 1140
DB 1101 CAGGCTCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAG 1160
QY 1141 CCGCTTGAAGCCACTGGGTCTTTCAGGAGTCACTGGAAGCTGGTGTGGCTGTCCCTGTG 1200
DB 1161 CCGCTTGAAGCCACTGGGTCTTTCAGGAGTCACTGGAAGCTGGTGTGGCTGTCCCTGTG 1220
QY 1201 CACTTCTGCACTGGGCTGGAAGTGGGCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 1260
DB 1221 CACTTCTGCACTGGGCTGGAAGTGGGCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 1280
QY 1261 CACTTGAAGGCTGTGGGCTGCTCCCTCTCTCCCTGCTCCAGTGTCCAGAGTCACTGAGGAGAG 1320
DB 1281 CACTTGAAGGCTGTGGGCTGCTCCCTCTCTCCCTGCTCCAGTGTCCAGAGTCACTGAGGAGAG 1340
QY 1321 GTCGTTGGAACATGAGACTGAGAGTGAAGGCTGAGGCTGAGATCTGAAACACACAGCCCTGTACT 1380
DB 1341 GTCGTTGGAACATGAGACTGAGAGTGAAGGCTGAGGCTGAGATCTGAAACACACAGCCCTGTACT 1400
QY 1381 TGGGTTGGCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
DB 1401 TGGGTTGGCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1460
QY 1441 CTGTCTTAGAGTGTGTGTAATCAGGAGGAGGATCAATTAATTTGTTTATTTCTCTC 1499
DB 1461 CTGTCTTAGAGTGTGTGTAATCAGGAGGAGGATCAATTAATTTGTTTATTTCTCTC 1519

US-10-102-806-218
; Sequence 218, Application US/10102806
; Publication No. US20030054421A1

| Query Match | Score 1481.4; | DB 14; | Length 1645; |
|-------------|---------------|--------|--------------|
| 98.68; | | | |

| | | | |
|----|-----|--|-----|
| QY | 1 | CGGCGTCGACGGGGCTTGTAGGTGTCCGGCTTTGCTGGCCACGCAAGCCTGATAAACATG | 60 |
| DB | 39 | CGGCGTCGACGGGGCTTGTAGGTGTCCGGCTTTGCTGGCCACGCAAGCCTGATAAACATG | 98 |
| QY | 61 | AAGCTCTATCTTTGTGGCCGGTGGTGGGCTGTTGTGCTGGTGCCTCCACAGTGAAGCAAC | 120 |
| DB | 99 | AAGCTCTATCTTTGTGGCTGTGGTGGGCTGTTGTGCTGGTGCCTCCACAGTGAAGCAAC | 158 |
| QY | 121 | AAGAGTTCTGAAGATACCGGTGCAAATGTGATCTGTCCACTTATAGAAACATCATGTGGG | 180 |
| DB | 159 | AAGAGTTCTGAAGATACCGGTGCAAATGTGATCTGTCCACTTATAGAAACATCATGTGGG | 218 |
| QY | 181 | CATATTTACAACCAAGATGTATCCGAAGAAGCATGCAACTGCTGCACCTGTGTGGAGGCC | 240 |
| DB | 219 | CACATTTACACAGAGATGTATCCGAAGAAGCATGCAACTGCTGCACCTGTGTGGAGGCC | 278 |
| QY | 241 | ATGCCAGTGCCTGGCCATGACGTTGGAGGCCCTACTGCTGCTGTGGAGTGCAGGTACGAG | 300 |
| DB | 279 | ATGCCAGTGCCTGGCCATGACGTTGGAGGCCCTACTGCTGCTGTGGAGTGCAGGTACGAG | 338 |
| QY | 301 | GAGCGACGACCCACACCAATCAAGGTTCATCTATCTACCTGCTCGGTGGTGGGTGCC | 360 |
| DB | 339 | GAGCGACGACCCACACCAATCAAGGTTCATCTATCTACCTGCTCGGTGGTGGGTGCC | 398 |
| QY | 361 | CTGTTCTCTACATGGCCCTCTCTGATGCTGGTGGACCTCTGATCCGAAGCCCGGATGCA | 420 |

| | | | | |
|----|--|------|---|------|
| D6 | | 399 | C T G T C T C A T A T G S C T C T O C T G A T G C T G F T G G A C C C T C T G A T C C G A A A G C C C G A T G C A | 458 |
| QY | | 421 | T A C A C T G A G C A A C T G C A C A A T G A G S A G A A T G A G A T G C T C G C T C T A T G C A G C A G C T | 480 |
| D6 | | 459 | I A V A C T G A C A A C T G C A C A N T A G A B A G A R A T G A G E M I S C T C S C T C T A T G C C A G A C A G C T | 518 |
| QY | | 481 | G C T G C A T C C C T C G S G S G A C C C C A G A A A C A C A G T C T G A G C G T F P G A A G G T G C C A G | 540 |
| D6 | | 519 | G C T G C A T C C C T C G S G S G A C C C C A G A A A C A C A G T C T G A G C G T F P G A A G G T G C C A G | 578 |
| QY | | 541 | A G S G T G G A A G C T G C A G T S C A G G A G C G G A A G A C A G T C T C G A T C G G A C A C A A G T G | 600 |
| D6 | | 579 | A G S G T G G A A G C T G C A G T S C A G G A G C G G A A G A C A G T C T C G A T C G G A C A C A A G T G | 638 |
| QY | | 601 | C T C A G C T A G A T G S G C T G T G T F T G S G T C A A G S C C C C A C A C C A T G C T G C C T G C C A C T C C | 660 |
| D6 | | 639 | C T C A G C T A G A T G S G C T G T G T F T G S G T C A A G S C C C C A C A C C A T G C T G C C T G C C A C T C C | 698 |
| QY | | 661 | A S G C T G S A A A G A C A G S S G C T A C T T C T C C H T C C C T T G S G T C C A G T C T C C C T T A A A A | 720 |
| D6 | | 699 | A S G C T G S A A A G A C A G S S G C T A C T T C T C C H T C C C T T G S G T C C A G T C T C C C T T A A A A | 758 |
| QY | | 721 | S C T G T G C A T T T T C C T C T T C C T A A C T T T A G A A T G T C T A C T T G S C T A T I T T G A | 780 |
| D6 | | 759 | G C C T G T G G C A T T T T C C T C T T C C C T A A C T T T A G A A T G T G T A C T T G S C T A T I T T G A | 818 |
| QY | | 781 | I T A G G A A G A G S G A T G T G S T C T C T G A T C T C T G T G T C T T T G S G T C T T T G S G T T G A A G | 840 |
| D6 | | 819 | I T A G G A A G A G S G A T G T G S T C T C T G A T C T C T G T G T C T T T G S G T C T T T G S G T T G A A G | 878 |
| QY | | 841 | G S A T G S S G A A G S C A G C C A G A A G S S A T G S A G A C A N T O G A G S G S C C T C A G A G T G S A T G | 900 |
| D6 | | 879 | G S A G S S G A A G S C A G C C A G A A G S S A T G S A G A C A T O G A G S G S C C T C A G A G T G S A T G | 938 |
| QY | | 901 | G S A T G T G T C T C T C T G S C C A C T C T T G C G C C T C C A G C T C T G A S T C T T G S S A T G T T G | 960 |
| D6 | | 939 | G S A T G T G T C T C T C T G S C C A C T C T T G C G C C T C C A G C T C T G A S T C T T G S S A T G T T G | 998 |
| QY | | 961 | I T A C C C T T G S A A G A T A A G S T G S G T C T C A G A A C T C A G T G T C G S A G A A A C A T G S C | 1020 |
| D6 | | 999 | I T A C C C T T G S A A G A T A A G S T G S G T C T C A G A A C T C A G T G T C G S A G A A A C A T G S C | 1058 |
| QY | | 1021 | C C A G C A T T C A C A T G T T T C T T T G C A G T G S T C - T T A T C A C A C C T C C C T C C A G C C | 1079 |
| D6 | | 1059 | C C A G C A T T C A C A T G T T T C T T T G C A G T G S T C - T T A T C A C A C C T C C C T C C A G C C | 1118 |
| QY | | 1080 | C C A G C C T C A G C C C A G C C C C A G C C T C A G C C T G A G A C A C T C T C A T G S G A G A G C T G S | 1139 |
| D6 | | 1119 | C C A G C C T C A G C C C A G C C C C A G C C T C A G C C T G A G A C A C T C T C A T G S G A G A G C T G S | 1178 |
| QY | | 1140 | G C C C C C T G A G C C C A C T G S G T C T T C A G S G T G C A C T G S A A G C T G S T T C S C T G T C C C T G T | 1199 |
| D6 | | 1179 | G C C C C C T G A G C C C A C T G S G T C T T C A G S G T G C A C T G S A A G C T G S T T C S C T G T C C C T G T | 1238 |
| QY | | 1200 | G C A C T T C T G C A C T G S G S G A T G S A G T G C C C A T G C A T A C T C T G C T G C G S G T C C C C T C A C C T | 1259 |
| D6 | | 1239 | G C A C T T C T G C A C T G S G S G A T G S A G T G C C C A T G C A T A C T C T G C T G C G S G T C C C C T C A C C T | 1298 |
| QY | | 1260 | G C A C T T G A G S G S T C T G S G C A T G C C C T C C T C C C C A G T G T C C A C A G T C A C T G A C C A G A C | 1319 |
| D6 | | 1299 | G C A C T T G A G S G S T C T G S G C A T G C C C T C C T C C C C A G T G T C C A C A G T C A C T G A C C A G A C | 1358 |
| QY | | 1320 | G S T G S T T G S A A C A T G A C A C T C G A G S C T G A G C T G A T C T G A A C A C A C A C A G C C C C T G C A C | 1379 |

Db 1359 GTTCGGTGGACATGAGACTCGAGGCTGAGGTGGATCTGGAACACACAGGCCCTGTAC 1418
Qy 1380 TTGGGTGGCTCTTGTCCCTGAACTTGGTGTACCACTGTCATGAGAGAGAAATTTTGTCC 1439
Db 1419 TTGGGTGGCTCTTGTCCCTGAACTTGGTGTACCACTGTCATGAGAGAGAAATTTTGTCC 1478
Qy 1440 TCTGTCTTAGAGTGTGTGTAAATCAGAGAGACATCAATTAATTTTATTTCTCTC 1499
Db 1479 TCTGTCTTAGAGTGTGTGTAAATCAGAGAGACATCAATTAATTTTATTTCTCTC 1538

RESULT 4

US-10-024-298A-150
; Sequence 150, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAH KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: GOEHI HONDA
; APPLICANT: SHUJI MORAMATSU
; APPLICANT: YUKIKO NAGANO
; TITLE OF INVENTION: NF-K B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP0089912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 150
; LENGTH: 1562
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (120)..(668)
US-10-024-298A-150

Query Match 98.7%; Score 1480; DB 14; Length 1562;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1494; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
Qy 1 GCGGCTGCAGCGGCTTGTAGGTGTCCGGCTTTGCTGGCCAGCAGAGCTGTGATAGCATG 60
Db 63 GCGGCTGCAGCGGCTTGTAGGTGTCCGGCTTTGCTGGCCAGCAGAGCTGTGATAGCATG 122
Qy 61 AAGCTCTATCTTTTGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 120
Db 123 AAGCTCTATCTTTTGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 182
Qy 121 AAGAGTCTGAGATATCGGTGCAATGCAATCTGTCCACCTTATAGACATCAGTGGG 180

Db 183 AAGAGTCTGAGATATCGGTGCAATGCAATCTGTCCACCTTATAGAAACATCAGTGGG 242
Qy 181 CATATTTACACACAGAAATGTATCCAGAAAGGACTGCAGTGCCTGCAGCTGGTGGAGGCC 240
Db 243 CACATTTACACACAGAAATGTATCCAGAAAGGACTGCAGTGCCTGCAGCTGGTGGAGGCC 302
Qy 241 ATGCCAGTGGCTGGCCATGAGCTGGAGGCTACTGCTGCTGTGGAGTGGAGTGGAGTGG 300
Db 303 ATGCCAGTGGCTGGCCATGAGCTGGAGGCTACTGCTGCTGTGGAGTGGAGTGGAGTGG 362
Qy 301 GAGGCGACACACACACACACACATCATTTGTCTCATCTACCTGTCCGTGGTGGGTC 360
Db 363 GAGGCGACACACACACACACATCATTTGTCTCATCTACCTGTCCGTGGTGGGTC 422
Qy 361 CTGTTGCTTACATGGGCTTCCTGATGCTGGAGCCCTCTGATCCGAAAGCCGATGCA 420
Db 423 CTGTTGCTTACATGGGCTTCCTGATGCTGGAGCCCTCTGATCCGAAAGCCGATGCA 482
Qy 421 TACACTGAGCAACTGCACATGAGGAGGAGATGAGTGTCTCTATGTCGACGAGCT 480
Db 483 TATACTGAGCAACTGCACATGAGGAGGAGATGAGTGTCTCTATGTCGACGAGCT 542
Qy 481 GCTGCATCCCTCGGGGACCCGAGCAACACACACTCTCTGAGGCTGTGGAGTGGCCAG 540
Db 543 GCTGCATCCCTCGGGGACCCGAGCAACACACACTCTCTGAGGCTGTGGAGTGGCCAG 602
Qy 541 CAGGCTGGAAGCTGCAAGTGCAGGAGCAGCGGAGAGACAGCTCTTCGATCGGCAAGATG 600
Db 603 CAGGCTGGAAGCTGCAAGTGCAGGAGCAGCGGAGAGACAGCTCTTCGATCGGCAAGATG 662
Qy 601 CTCAGCTAGATGGGCTGGTGTGGTGGTCAAAGCCGCAACACATGGTGGCAGCTTCC 660
Db 663 CTCAGCTAGATGGGCTGGTGTGGTCAAAGCCGCAACACATGGTGGCAGCTTCC 722
Qy 661 AGGCTGAGCAAAAGCAGGGGCTACTTCTCCCTTCCTCGGTTCCAGTCTCCCTTTAAA 720
Db 723 AGGCTGAGCAAAAGCAGGGGCTACTTCTCCCTTCCTCGGTTCCAGTCTCCCTTTAAA 782
Qy 721 GCTGTGGCAATTTTCT 780
Db 783 GCTGTGGCAATTTTCT 842
Qy 781 TTAGGAGAGAGGATGTGGTCTCTGATCTCTGTGTCTCTCTCTCTCTCTCTCTCTCTCT 840
Db 843 TTAGGAGAGAGGATGTGGTCTCTGATCTCTGTGTCTCTCTCTCTCTCTCTCTCTCTCT 902
Qy 841 GATGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
Db 903 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 962
Qy 901 GATCTGTCT 960
Db 963 GATCTGTCT 1022
Qy 961 TTACCTTGGAGATAAAGCTGGGCTTTCAGGAACTCAGTGTCTGGGAGGAGGAGGAGGAG 1020
Db 1023 TTACCTTGGAGATAAAGCTGGGCTTTCAGGAACTCAGTGTCTGGGAGGAGGAGGAGGAG 1082
Qy 1021 CCAGCATTCAGCATGTGTCT 1079
Db 1083 CCAGCATTCAGCATGTGTCT 1142
Qy 1080 CCAAGGCTCAGGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCA 1139

| | Matches 1494; | Conservative | 0; | Mismatches | 5; | Indels | 1; | Gaps | 1; |
|----|---------------|--------------|--|------------|----|--------|----|------|----|
| QY | 1 | GC | GCCTCAGCAGCGGGCTGTGTAGGTGTCCGGCTTTGCTGGCCACGAAAGCCTGATAAAGCATG | 60 | | | | | |
| DB | 63 | GC | GGCTCAGCAGCGGGCTGTGTAGGTGTCCGGCTTTGCTGGCCACGAAAGCCTGATNAAGCATG | 122 | | | | | |
| QY | 65 | AA | GGCTCTTATCTTTTGGTGGCCGTGTGGGTGTTTGGTGGTGGCCCGCAGCTGAAGCCAAAC | 120 | | | | | |
| DB | 123 | AA | GGCTCTTATCTTTTGGTGGCTGTGGGTGTTTGGTGGTGGCCCGCAGCTGAAGCCAAAC | 182 | | | | | |
| QY | 121 | AA | GAGTTCTTGAAAGATACCGGTGCAAAATGCATCTGCACCTTATAGAAACATCACTAGTGGG | 180 | | | | | |
| DB | 183 | AA | GAGTTCTTGAAAGATACCGGTGCAAAATGCATCTGCACCTTATAGAAACATCACTAGTGGG | 242 | | | | | |
| QY | 161 | CA | TATTTACAAACCAAGATGTATCCGAGAAAGCATGCAACTGCTGCACGTGGTGGAGCC | 240 | | | | | |
| DB | 243 | CA | TATTTACAAACCAAGATGTATCCGAGAAAGCATGCAACTGCTGCACGTGGTGGAGCC | 302 | | | | | |
| QY | 241 | AT | CCAGTGGTGGTGGCCATGAGTGGAGGCTACTGCTGCTGTGGAGTGCAGGTACGAG | 300 | | | | | |
| DB | 303 | AT | CCAGTGGTGGTGGCCATGAGTGGAGGCTACTGCTGCTGTGGAGTGCAGGTACGAG | 362 | | | | | |
| QY | 301 | GA | CGGCAACCAACCAACCAAGTCTATATTTGATCTTACCTGTCCGTGGTGGTGGCC | 360 | | | | | |
| DB | 363 | GA | CGGCAACCAACCAACCAAGTCTATATTTGATCTTACCTGTCCGTGGTGGTGGCC | 422 | | | | | |

RESULT 5

| | | |
|-----|--|-----|
| 423 | CTTGTGCTCTACATGGCCTTCCTGATGCTGGTGAGACCTCTGATCGGAAACGCGGATGCA | 482 |
| QY | | |
| 424 | TACATCTGAGCAACTGCACATGAGGAGGAGATGAGGATGCTCGCTCTATGGCAGCAGCT | 480 |
| QY | | |
| 425 | TATCTGAGCAACTGCACATGAGGAGGAGATGAGATGCTCGCTCTATGGCAGCAGCT | 542 |
| DB | | |
| 426 | GCTGCATCCTTCGCGGGAGACCCGAGCAACACAGTCTCTGGAGGCTGTGGAGGTGCCAG | 602 |
| QY | | |
| 427 | GCTGCATCCTTCGCGGGAGACCCGAGCAACACAGTCTCTGGAGGCTGTGGAGGTGCCAG | 540 |
| DB | | |
| 428 | CAGCGGTGGAGAGCTGCAGGTCGAGAGCAGCGGAGAGACAGTCTTCGATCGGCAAGATG | 600 |
| QY | | |
| 429 | CAGCGGTGGAGAGCTGCAGGTCGAGAGCAGCGGAGAGACAGTCTTCGATCGGCAAGATG | 662 |
| DB | | |
| 430 | CTCAGCTAGATGGGCTGTGTGGTTCGAGGCCCCACACACATGGCTGCCAGCTTCC | 660 |
| QY | | |
| 431 | CTCAGCTAGATGGGCTGTGTGGTTCGAGGCCCCACACACATGGCTGCCAGCTTCC | 722 |
| DB | | |
| 432 | AGGCTGGACAAAGCAGGGGGTACTTCTCCCTTCCTCGGTTCCAGTCTTCCCTTTAAA | 720 |
| QY | | |
| 433 | AGGCTGGACAAAGCAGGGGGTACTTCTCCCTTCCTCGGTTCCAGTCTTCCCTTTAAA | 782 |
| DB | | |
| 434 | GCTCTGGCACTTTTCTCCTCTCTCCCTAACTTTAGAAATGTTGACTGGCTATTTTGA | 780 |
| QY | | |
| 435 | GCTCTGGCACTTTTCTCCTCTCTCCCTAACTTTAGAAATGTTGACTGGCTATTTTGA | 842 |
| DB | | |
| 436 | TTAGGGAAGAGGATGTGGTCTCTGATCTCTGTTCTTCCTGGGCTCTTGGGGTTGAAG | 840 |
| QY | | |
| 437 | TTAGGGAAGAGGATGTGGTCTCTGATCTCTGTTCTTCCTGGGCTCTTGGGGTTGAAG | 902 |
| DB | | |
| 438 | GGATGGGGAAGGCGAGGCCCAAGGGAATGGAGACATCGAGCGGGCTCTCAGAGATGGATG | 900 |
| QY | | |

[illegible]

Db 963 CGAATCTGTCTCTCTGGCTCCACTCTTGGCGCTTCAGCTCTGAGTCTTGGGAATGTG 1022
Qy 961 TTACCTTGGGAATAAGAGTGGGTCTTCCAGGAATCAGTGTCTGGGAGGAAAGCATGGC 1020
Db 1023 TTACCTTGGGAATAAGAGTGGGTCTTCCAGGAATCAGTGTCTGGGAGGAAAGCATGGC 1082
Qy 1021 CCAGATTCAGCATGTGTCTTCTTCTGAGTGTTC-TTATCACCACTCTCCCTCCAGCC 1079
Db 1083 CCAGCATTCAGCATGTGTCTTCTTCTGAGTGTTC-TTATCACCACTCTCCCTCCAGCC 1142
Qy 1080 CCAGCCCTCAGCCGCCAGCCGCCAGCTCCAGCCCTCAGGACAGCTCTGATGGAGAGCTGG 1139
Db 1143 CCAGCCCTCAGCCGCCAGCCGCCAGCTCCAGCCCTCAGGACAGCTCTGATGGAGAGCTGG 1202
Qy 1140 GCCCCTCAGCCGCCAGCTGGGTCTTCCAGGGTGCAGTGGAGCTGGTGTGCTGTCTCCCTGT 1199
Db 1203 GCCCCTCAGCCGCCAGCTGGGTCTTCCAGGGTGCAGTGGAGCTGGTGTGCTGTCTCCCTGT 1262
Qy 1200 GCATCTCTGCACTGGGGCATGGAGTGGCCATGCATCTCTGCTGGGGTCCCTGACCT 1259
Db 1263 GCATCTCTGCACTGGGGCATGGAGTGGCCATGCATCTCTGCTGGGGTCCCTGACCT 1322
Qy 1260 GCATCTGGGGGTCTGGGCACTGCTCTCTCTCCCACTGTCACAGTCACTGAGCCAGAC 1319
Db 1323 GCATCTGGGGGTCTGGGCACTGCTCTCTCTCCCACTGTCACAGTCACTGAGCCAGAC 1382
Qy 1320 GGTGGGTGGGAACATGAGATCTCGAGGCTGAGGTGGATCTGAAACACACAGCCCTGTAC 1379
Db 1383 GGTGGGTGGGAACATGAGATCTCGAGGCTGAGGTGGATCTGAAACACACAGCCCTGTAC 1442
Qy 1380 TTGGGTGCTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1439
Db 1443 TTGGGTGCTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1502
Qy 1440 TCTTGTCTTAGAGTTGTGTGTAATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1499
Db 1503 TCTTGTCTTAGAGTTGTGTGTAATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1562

RESULT 6

US-10-153-668-93
; Sequence 93, Application US/10153668
; Publication No. US20030092616A1
; GENERAL INFORMATION:
; APPLICANT: HONDA, Goichi
; APPLICANT: MATSUDA, Akio
; APPLICANT: MURAMATSU, Shuji
; APPLICANT: ISHIZAWA, Kenya
; TITLE OF INVENTION: STAT6 Activating Gene
; FILE REFERENCE: 1254-0207P
; CURRENT APPLICATION NUMBER: US/10/153,668
; CURRENT FILING DATE: 2002-03-24
; PRIOR APPLICATION NUMBER: US 60/293,172
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/316,031
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/328,403
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: JP 2001-157043
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: JP 2001-260681
; PRIOR FILING DATE: 2001-08-30

; PRIOR APPLICATION NUMBER: JP 2001-313175
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 488
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (63)...(611)
US-10-153-668-93

Query Match 98.6%; Score 1478; DB 14; Length 1503;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1492; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy 1 GCGGCTGCAGGGGCTTGTAGGTGTCCGGCTTTGCTGGCCGAGCAAGCTGATGAAGCATG 60
Db 6 GCGGCTGCAGGGGCTTGTAGGTGTCCGGCTTTGCTGGCCGAGCAAGCTGATGAAGCATG 65
Qy 61 AAGCTCTTATCTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
Db 66 AAGCTCTTATCTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 125
Qy 121 AAGGTTCTGAAGATATCCGGTGCATATGATCTGTCCACCTTATAGAAGCATCAAGTGG 180
Db 126 AAGGTTCTGAAGATATCCGGTGCATATGATCTGTCCACCTTATAGAAGCATCAAGTGG 185
Qy 181 CATATTTACACACAGAAATGATCCAGAGGAGCTGCAACTGCTGCACTGCTGCACTGCTG 240
Db 186 CATATTTACACACAGAAATGATCCAGAGGAGCTGCAACTGCTGCACTGCTGCACTGCTG 245
Qy 241 ATGCCAGTGGCTGGCCATGAGCTGGAGGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 246 ATGCCAGTGGCTGGCCATGAGCTGGAGGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 305
Qy 301 GAGCGCAGCACCACCAACCAATCAAGGTCATCATCTCATCTCATCTCATCTCATCTCATCT 360
Db 306 GAGCGCAGCACCACCAACCAATCAAGGTCATCATCTCATCTCATCTCATCTCATCTCATCT 365
Qy 361 CTGTTGCTCTACATGGCTTCTTCTGATGTGGTGGACCTCTGATCCGAAAGCCGATGCA 420
Db 366 CTGTTGCTCTACATGGCTTCTTCTGATGTGGTGGACCTCTGATCCGAAAGCCGATGCA 425
Qy 421 TACTAGCAGCACTGCACATGAGAGGAGTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 480
Db 426 TACTAGCAGCACTGCACATGAGAGGAGTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 485
Qy 481 GCTGATCCCTCGGGGACCCCGAGCAACACAGTCTGAGAGGCTGTGAGAGGTCGACAG 540
Db 486 GCTGATCCCTCGGGGACCCCGAGCAACACAGTCTGAGAGGCTGTGAGAGGTCGACAG 545
Qy 541 CAGCGGTGGAAGCTGAGGTGAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
Db 546 CAGCGGTGGAAGCTGAGGTGAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 605
Qy 601 CTCAGTAGATGGGCTGGTGTGGTGGGTCAAGGCCCCCAACCATGGCTGGCAGGCTTCC 660
Db 606 CTCAGTAGATGGGCTGGTGTGGTGGGTCAAGGCCCCCAACCATGGCTGGCAGGCTTCC 665
Qy 661 AGGCTGAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720

RESULT 7
US-09-946-374-67
; Sequence 67, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc

| | |
|-----------------------------|--|
| APPLICANT: | Batcz, Dan L. |
| APPLICANT: | Ferrara, Napoleone |
| APPLICANT: | Fong, Sherman |
| APPLICANT: | Gao, Wei-Qiang |
| APPLICANT: | Goddard, Audrey |
| APPLICANT: | Godowski, Paul J. |
| APPLICANT: | Grimaldi, Christopher J. |
| APPLICANT: | Gurney, Austin L. |
| APPLICANT: | Hillan, Kenneth J. |
| APPLICANT: | Pan, James |
| APPLICANT: | Paoni, Nicholas F. |
| APPLICANT: | Roy, Margaret Ann |
| APPLICANT: | Smith, Victoria |
| APPLICANT: | Stewart, Timothy A. |
| APPLICANT: | Tumas, Daniel |
| APPLICANT: | Watanabe, Colin K. |
| APPLICANT: | Williams, P. Mickey |
| APPLICANT: | Wood, William I. |
| TITLE OF INVENTION: | Acids and Transmembrane Polypeptides and Nucleic |
| TITLE OF INVENTION: | Acids Encoding the Same |
| FILE REFERENCE: | P2830P1C1 |
| CURRENT APPLICATION NUMBER: | US/09/946,374 |
| CURRENT FILING DATE: | 2001-09-04 |
| PRIOR APPLICATION NUMBER: | 60/098716 |
| PRIOR FILING DATE: | 1998-09-01 |
| PRIOR APPLICATION NUMBER: | 60/098723 |
| PRIOR FILING DATE: | 1998-09-01 |
| PRIOR APPLICATION NUMBER: | 60/098749 |
| PRIOR FILING DATE: | 1998-09-01 |
| PRIOR APPLICATION NUMBER: | 60/098750 |
| PRIOR FILING DATE: | 1998-09-01 |
| PRIOR APPLICATION NUMBER: | 60/098803 |
| PRIOR FILING DATE: | 1998-09-02 |
| PRIOR APPLICATION NUMBER: | 60/098821 |
| PRIOR FILING DATE: | 1998-09-02 |
| PRIOR APPLICATION NUMBER: | 60/098843 |
| PRIOR FILING DATE: | 1998-09-02 |
| PRIOR APPLICATION NUMBER: | 60/099536 |
| PRIOR FILING DATE: | 1998-09-09 |
| PRIOR APPLICATION NUMBER: | 60/099596 |
| PRIOR FILING DATE: | 1998-09-09 |
| PRIOR APPLICATION NUMBER: | 60/099598 |
| PRIOR FILING DATE: | 1998-09-09 |
| PRIOR APPLICATION NUMBER: | 60/099602 |
| PRIOR FILING DATE: | 1998-09-09 |
| PRIOR APPLICATION NUMBER: | 60/099642 |
| PRIOR FILING DATE: | 1998-09-09 |
| PRIOR APPLICATION NUMBER: | 60/099741 |
| PRIOR FILING DATE: | 1998-09-10 |
| PRIOR APPLICATION NUMBER: | 60/099754 |
| PRIOR FILING DATE: | 1998-09-10 |
| PRIOR APPLICATION NUMBER: | 60/099763 |
| PRIOR FILING DATE: | 1998-09-10 |
| PRIOR APPLICATION NUMBER: | 60/099792 |
| PRIOR FILING DATE: | 1998-09-10 |
| PRIOR APPLICATION NUMBER: | 60/099808 |
| PRIOR FILING DATE: | 1998-09-10 |
| PRIOR APPLICATION NUMBER: | 60/099812 |
| PRIOR FILING DATE: | 1998-09-10 |
| PRIOR APPLICATION NUMBER: | 60/099815 |
| PRIOR FILING DATE: | 1998-09-10 |
| PRIOR APPLICATION NUMBER: | 60/099816 |
| PRIOR FILING DATE: | 1998-09-10 |

; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807

Query Match 98.3%; Score 1473.6; DB 10; Length 1564;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1476; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 20 AGGTGTCGGGCTTTGGTGGCCCGAGAGCTGATAGATGAAGCTCTTATCTTTGGTGG 79
DB 84 AGGTGTCGGGCTTTGGTGGCCCGAGAGCTGATAGATGAAGCTCTTATCTTTGGTGG 143
QY 80 CGGTGTCGGGCTTTGGTGGCCCGAGAGCTGATAGATGAAGCTCTTATCTTTGGTGG 139
DB 144 CTGTGTCGGGCTTTGGTGGCCCGAGAGCTGATAGATGAAGCTCTTATCTTTGGTGG 203
QY 140 GGTGCAATGCAATCTGCACTTATAGAAACATCAATGAGGATATTTACACCAAGATG 199
DB 264 GGTGCAATGCAATCTGCACTTATAGAAACATCAATGAGGATATTTACACCAAGATG 263
QY 200 TATCCAGAAAGACTGCACTGCTGCAAGTGGTGGAGCCCATGGCAGTGGCTGGCCATG 259
DB 264 TATCCAGAAAGACTGCACTGCTGCAAGTGGTGGAGCCCATGGCAGTGGCTGGCCATG 323
QY 260 AGGTGAGGCTTACTGCTGCTGTGGAGTGCAGTACGAGAGGAGCGACACACCA 319
DB 324 AGGTGAGGCTTACTGCTGCTGTGGAGTGCAGTACGAGAGGAGCGACACACCA 383
QY 320 TCAAGTGCATCATTTGATCATCTACTGCTGGTGGTGGCTGCTGCTGCTGCTGCT 379
DB 384 TCAAGTGCATCATTTGATCATCTACTGCTGGTGGTGGCTGCTGCTGCTGCTGCT 443
QY 380 TCTGATGCTGGTGGAGCTGCTGATCCGAAAGCCGATGATACACTGAGCAACTGCACA 439
DB 444 TCTGATGCTGGTGGAGCTGCTGATCCGAAAGCCGATGATACACTGAGCAACTGCACA 503
QY 440 ATGAGGAGAGATGAGGATGCTGCTGCTATGGAGAGAGCTGCTGCTGCTGCTGCTGCT 499
DB 504 ATGAGGAGAGATGAGGATGCTGCTGCTATGGAGAGAGCTGCTGCTGCTGCTGCTGCT 563
QY 500 CCGGAGCAACACAGTCTGAGAGCTGTGGAGGTGCGCAGAGCGGTGGAGCTGCAGG 559
DB 564 CCGGAGCAACACAGTCTGAGAGCTGTGGAGGTGCGCAGAGCGGTGGAGCTGCAGG 623
QY 560 TGCAGAGCAACGAGAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 619
DB 624 TGCAGAGCAACGAGAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 683
QY 620 GTGGTGGTGAAGGCGCCAGACCAATGGCTGCCAGCTTCCAGGCTGAGCAAGAGAGG 679
DB 684 GTGGTGGTGAAGGCGCCAGACCAATGGCTGCCAGCTTCCAGGCTGAGCAAGAGAGG 743
QY 680 GCTACTTCTCCCTCCCTGGTCCAGTCTTCCCTTAAAGGCTGTGGCAATTTTCCTC 739
DB 744 GCTACTTCTCCCTCCCTGGTCCAGTCTTCCCTTAAAGGCTGTGGCAATTTTCCTC 803
QY 740 CTCTCTCCCTTAAAGGATGTTGTTACTTGGCTATTTGATAGGAGAGAGGATGTTGG 799
DB 804 CTCTCTCCCTTAAAGGATGTTGTTACTTGGCTATTTGATAGGAGAGAGGATGTTGG 863
QY 800 TCTCTGATCTCTGTTGCTCTGCTGGTCTTTGGGCTTGAAGGATGAGGAGAGGCA 859

DB 864 TCTCTGATCTCTGTTCTTCTTGGGCTTTGGGCTTGAAGGAGGAGGAGGAGGAGGCA 923
QY 860 GAAGGAGATGAGACATTCAGAGGCGCTCAGAGTGAATGAGATCTGTTCTCTCTGGCT 919
DB 924 GAAGGAGATGAGACATTCAGAGGCGCTCAGAGTGAATGAGATCTGTTCTCTCTGGCT 983
QY 920 CACTCTTGGCGCTTCCAGCTCTGAGTCTTGGGATGTTGTTACCTTGGAGAAAG 979
DB 984 CACTCTTGGCGCTTCCAGCTCTGAGTCTTGGGATGTTGTTACCTTGGAGAAAG 1043
QY 980 CTGGGCTTTCAGAACTCAGTGTCTGGGAGAAAGATGAGGAGGAGGAGGAGGAGGATGTT 1039
DB 1044 CTGGGCTTTCAGAACTCAGTGTCTGGGAGAAAGATGAGGAGGAGGAGGAGGATGTT 1103
QY 1040 CTTTCTGAGTGGTCTTATCACCACCTCCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGG 1099
DB 1104 CTTTCTGAGTGGTCTTATCACCACCTCCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGG 1163
QY 1100 CAGGCTCCAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1159
DB 1164 CAGGCTCCAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1223
QY 1160 CTTCAAGGCTGAGTGAAGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1219
DB 1224 CTTCAAGGCTGAGTGAAGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1283
QY 1220 TGAAGTGGGATGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1279
DB 1284 TGAAGTGGGATGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1343
QY 1280 GTCCCTCTCTCCAGTGTCCAGAGTCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1339
DB 1344 GTCCCTCTCTCCAGTGTCCAGAGTCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1403
QY 1340 TGAAGTGGGATGCACTGCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1399
DB 1404 TGAAGTGGGATGCACTGCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1463
QY 1400 GAAGTGGGATGCACTGCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1459
DB 1464 GAAGTGGGATGCACTGCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1523
QY 1460 TGAAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1499
DB 1524 TGAAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1563

RESULT 8
US-10-206-915-245
; Sequence 245, Application US/10206915
; Publication No. US20040029221A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.

| | | |
|------|---|------|
| 1340 | TGAGCGCTGACCTGGATCTGAACACACAGCCCTGTACTTGGTTGCCTCTTGCCCT | 1399 |
| QY | | |
| D6 | | |
| 1404 | TGAGCGCTGACCTGGATCTGAACACACAGCCCTGTACTTGGTTGCCTCTTGCCCT | 1463 |
| D6 | | |
| 1480 | GAACTTCGTCTGACCAAGTGCATGSAGAGAAAATTTGGCTCTGTGCTTAGAATTCTGTG | 1459 |
| QY | | |
| D6 | | |
| 1464 | GAACTTCGTCTGACCAAGTGCATGSAGAGAAAATTTGGCTCTGTGCTTAGAATTCTGTG | 1523 |
| QY | | |
| 1460 | TAAATCAAGSAAGCCCATTAANTTTGTTTTATTCTCTC | 1499 |
| QY | | |
| D6 | | |
| 1524 | TAAATCAAGSAAGCCCATTAANTTTGTTTTATTCTCTC | 1563 |
| D6 | | |

RESULT 9

```

US-10-199-670-245
/ Sequence 245, Application US/10199670
/ Publication No. US20040033560A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3430RIC401
/ CURRENT APPLICATION NUMBER: US/10/199,670
/ CURRENT FILING DATE: 2002-07-19
/ PRIOR APPLICATION NUMBER: 10/052586
/ PRIOR FILING DATE: 2002-01-15
/ PRIOR APPLICATION NUMBER: 60/059263
/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/059266
/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/062250
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/063120
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/063121
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/063486
/ PRIOR FILING DATE: 1997-10-21
/ PRIOR APPLICATION NUMBER: 60/063540
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/063541
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/063544
/ PRIOR FILING DATE: 1997-10-28
/ Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 245
/ LENGTH: 1564
/ TYPE: DNA
/ ORGANISM: Homo Sapien
US-10-199-670-245

```

Query Match 98.3% Score 1473.6 DB 12 Length 1564

QY 920 CCACCTCTGCGGCTTCCACGCTCTGAGTCTTGGAAAGTGTACCTTGGAGATAG 979
Db 984 CCACCTCTGCGGCTTCCACGCTCTGAGTCTTGGAAAGTGTACCTTGGAGATAG 1043
QY 980 CTGGGCTTTCAGGAACCTGAGTCTGCGGAAAGCATGCGCCAGCATGTGT 1039
Db 1044 CTGGGCTTTCAGGAACCTGAGTCTGCGGAAAGCATGCGCCAGCATGTGT 1103
QY 1040 CTTTCTGAGTGTGTCTTATCAGCAGCTCTCCAGCCAGGCGCTCAGCCGAGCC 1099
Db 1104 CTTTCTGAGTGTGTCTTATCAGCAGCTCTCCAGCCAGGCGCTCAGCCGAGCC 1163
QY 1100 CCAGCTCCAGGCTTGGAGCAGCTCTGATGGGAGAGCTGGGCGCCCTGAGCCAGCTGGGT 1159
Db 1164 CCAGCTCCAGGCTTGGAGCAGCTCTGATGGGAGAGCTGGGCGCCCTGAGCCAGCTGGGT 1223
QY 1160 CTTTCAAGGCTGAGGAGCTGAGTGTGTCTGCGGCTTGGAGCTGTGAGCTGGGCA 1219
Db 1224 CTTTCAAGGCTGAGGAGCTGAGTGTGTCTGCGGCTTGGAGCTGTGAGCTGGGCA 1283
QY 1220 TGGAGTGGCCAGTACCTCTGCTGCCGCTTCCCTCAGCTGCACTTGGGCTCTGGGCA 1279
Db 1284 TGGAGTGGCCAGTACCTCTGCTGCCGCTTCCCTCAGCTGCACTTGGGCTCTGGGCA 1343
QY 1280 GTCCCTCTCTCCAGTGTCCACAGTCTGAGCCAGAGCTGGGCTTGGAGCATGAGAC 1339
Db 1344 GTCCCTCTCTCCAGTGTCCACAGTCTGAGCCAGAGCTGGGCTTGGAGCATGAGAC 1403
QY 1340 TCGAGCTGAGGCTGAGTCTGAGCAGCAGCTGAGGCTTGGGCTTGGGCTCTGCTGCT 1399
Db 1404 TCGAGCTGAGGCTGAGTCTGAGCAGCAGCTGAGGCTTGGGCTTGGGCTCTGCTGCT 1463
QY 1400 GACTCTGCTTACAGTGTGAGTGTGAGGAGAAATTTGTCTCTGCTCTAGAGTGTGTG 1459
Db 1464 GACTCTGCTTACAGTGTGAGTGTGAGGAGAAATTTGTCTCTGCTCTAGAGTGTGTG 1523
QY 1460 TAAATCAAGGAAGCAATCAATTAATTTTATTTCTCTC 1499
Db 1524 TAAATCAAGGAAGCAATCAATTAATTTTCTCTC 1563

RESULT 10

US-10-201-658-245
; Sequence 245, Application US/10201858
; Publication No. US2004003837A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C464
; CURRENT APPLICATION NUMBER: US/10/201,858
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 245
; LENGTH: 1564
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-201-658-245

Query Match 98.3%; Score 1473.6; DB 12; Length 1564;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1476; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 20 AGGTGTCGGCTTGTGTCGCCAGCAGCTGATAGCAAGAGCTCTATCTTGTGG 79
Db 84 AGGTGTCGGCTTGTGTCGCCAGCAGCTGATAGCAAGAGCTCTATCTTGTGG 143
QY 80 CGGTGTCGGCTTGTGTCGCCAGCAGCTGATAGCAAGAGCTCTATCTTGTGG 139
Db 144 CTGTGTCGGCTTGTGTCGCCAGCAGCTGATAGCAAGAGCTCTATCTTGTGG 203
QY 140 GGTGCAATGCATCTGTCCACCTTATAGAAACATCAGTGGCATATTTACACCAATG 199
Db 204 GGTGCAATGCATCTGTCCACCTTATAGAAACATCAGTGGCATATTTACACCAATG 263
QY 200 TATCCAGAGGACTGCAACTGCTGCAGTGGTGGAGCCCATGCCAGTGCCTGGCCATG 259
Db 264 TATCCAGAGGACTGCAACTGCTGCAGTGGTGGAGCCCATGCCAGTGCCTGGCCATG 323
QY 260 ACGTGGAGGCTACTGCTGCTGTGCGAGTGCAGTAAGAGAGGCGCAGCACCAACCA 319
Db 324 ACGTGGAGGCTACTGCTGCTGTGCGAGTGCAGTAAGAGAGGCGCAGCACCAACCA 383
QY 320 TCAAGGTCAITCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 379
Db 384 TCAAGGTCAITCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 443
QY 380 TCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 439
Db 444 TCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 503
QY 440 ATGAGGAGAGCAATGAGGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 499
Db 504 ATGAGGAGAGCAATGAGGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 563

Qy 1460 TAATCAAGGAAGCATCAATTAATGTTTATTCTCTC 1499
|||||

D6 1524 TAATCAAGGAAGCATCAATTAATGTTTATTCTCTC 1563

US-10-205-890-245

| | Query Match | 98.3% | Score 1473.6 | DB 12 | Length 1564 |
|----|-----------------------|---|--------------|-------|-------------|
| | Best Local Similarity | 99.7% | Pred. No. 0 | | |
| | Matches 1476 | Conservative | Mismatches | 4 | Gaps 0 |
| QY | 20 | AGGTGTCGCGCTTCTTGGCCGACGACGCTGATGACCTGACCTCTATCTTTGGTGG | | | |
| DB | 84 | AGGTGTCGCGCTTCTTGGCCGACGACGCTGATGACCTGACCTCTATCTTTGGTGG | | | |

Query Match 98.3%; Score 1473.6; DB 12; Length 1564;

Best Local Similarity 99.7%; Pred. No. 0;

| | | | | | | | | | |
|---------|-------|--------------|----|------------|----|--------|----|------|----|
| Matches | 1476; | Conservative | 0; | Mismatches | 4; | Indels | 0; | Gaps | 0; |
|---------|-------|--------------|----|------------|----|--------|----|------|----|

20 AGGTGTCGGCTTTGCTGGCCAGCAAGCTGATAAGCATGAAGCTCTATCTTTGGTGG 79

B4 AGSTGTCCGCTTCTCGCCCGCCAGCAGCCATGACCATTCATTTCTTCCGC 143

84 AGGTTGTCGCGCTTTGCTGGCCAGCAAGCCTGATAAGCATGAAGCTCTTATCTTTGGTGG 143

; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 245
; LENGTH: 1564
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-208-024-245

Query Match 98.3%; Score 1473.6; DB 12; Length 1564;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1476; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 20 AGGTGTCGGGTTTGGTGGCCAGCAAGCCTGATAGCATGAGCTCTTATCTTTGGTGG 79
DB 84 AGTGTTCGGGCTTTGCTGGCCAGCAAGCCTGATAGCATGAGCTCTTATCTTTGGTGG 143
QY 80 CGGTGTGGGTTTGGTGGTGGCCAGCAAGCTGATAGCATGAGCTCTTATCTTTGGTGG 139
DB 144 CTGTGTGGGTTTGGTGGTGGCCAGCAAGCTGATAGCATGAGCTCTTATCTTTGGTGG 203
QY 140 GGTGCAATGCACTGTCCACCTTATAGAAACATCACTGGGCAATATTAGACCAAGATG 199
DB 204 GGTGCAATGCACTGTCCACCTTATAGAAACATCACTGGGCAATATTAGACCAAGATG 263
QY 200 TATCCAGAAAGCACTGTCCACCTTATAGAAACATCACTGGGCAATATTAGACCAAGATG 259
DB 264 TATCCAGAAAGCACTGTCCACCTTATAGAAACATCACTGGGCAATATTAGACCAAGATG 323
QY 260 ACCTGGAAGGCTTACTGCTGTGTGGGAGTGCAGGTACGAGGAGGCGAGCAACCAACCA 319
DB 324 ACCTGGAAGGCTTACTGCTGTGTGGGAGTGCAGGTACGAGGAGGCGAGCAACCAACCA 383
QY 320 TCAAGGTCACTCAATGTCATCTACTGCTGTGGTGGTGGCTGTGTGTGTGTGTGTGTGT 379
DB 384 TCAAGGTCACTCAATGTCATCTACTGCTGTGGTGGTGGCTGTGTGTGTGTGTGTGTGT 443
QY 380 TCCTGATGCTGGTGGAGCCTCTGATCCGAAAGCGCGGATGCATACACTGAGCAACTGCACA 439
DB 444 TCCTGATGCTGGTGGAGCCTCTGATCCGAAAGCGCGGATGCATACACTGAGCAACTGCACA 503
QY 440 ATGAGGAGGAGATGAGGATGCTGCTCTATGGGAGAGCTGCTGATGCTGCTGGGAGC 499
DB 504 ATGAGGAGGAGATGAGGATGCTGCTCTATGGGAGAGCTGCTGATGCTGCTGGGAGC 563
QY 500 CCGGAGCAAAACACAGTCTGGAGGCTGTGGAGGCTGCGAGGCTGCGAGGCTGCGAGG 559
DB 564 CCGGAGCAAAACACAGTCTGGAGGCTGTGGAGGCTGCGAGGCTGCGAGGCTGCGAGG 623
QY 560 TGCAGGAGCAGGAGGAGAGCTCTTCGATCGGCAACAGATGCTCAGCTAGATGGGCTGGT 619
DB 624 TGCAGGAGCAGGAGGAGAGCTCTTCGATCGGCAACAGATGCTCAGCTAGATGGGCTGGT 683

QY 620 GTGGTGGGTCAGAGGCCCAACACCATGGCTGCCAGCTTCCAGGCTGSAACAAAGAGGGG 679
DB 684 GTGGTGGGTCAGAGGCCCAACACCATGGCTGCCAGCTTCCAGGCTGSAACAAAGAGGGG 743
QY 680 GCTACTTCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCC 739
DB 744 GCTACTTCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCC 803
QY 740 CTTCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCC 799
DB 804 CTTCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCC 863
QY 800 TCTCTGATCT 859
DB 864 TCTCTGATCT 923
QY 860 GAAGGAGATGAGAGCATTCGAGGCGGCTCAGGAGTGGATGCGATCTGTCTCTCTCTCTCTCT 919
DB 924 GAAGGAGATGAGAGCATTCGAGGCGGCTCAGGAGTGGATGCGATCTGTCTCTCTCTCTCTCT 983
QY 920 CCACTCTTGGCGCTTCCAGCTCTGAGTCTTGGGAAATGTTTACCTTGGAAAGATAAG 979
DB 984 CCACTCTTGGCGCTTCCAGCTCTGAGTCTTGGGAAATGTTTACCTTGGAAAGATAAG 1043
QY 980 CTGGGCTTCCAGGACCTCAGTGTCTGGGAGAAAGCATGGCCAGCATTCAGCATGTGT 1039
DB 1044 CTGGGCTTCCAGGACCTCAGTGTCTGGGAGAAAGCATGGCCAGCATTCAGCATGTGT 1103
QY 1040 CTTTCTGCACTGTCTTATCACCCTTCCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1099
DB 1104 CTTTCTGCACTGTCTTATCACCCTTCCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1163
QY 1100 CCAAGTCCAGGCTTCCAGGACCTCTGATGGGAGAGCTGGGCGCCCTGAGCCACTGGGT 1159
DB 1164 CCAAGTCCAGGCTTCCAGGACCTCTGATGGGAGAGCTGGGCGCCCTGAGCCACTGGGT 1223
QY 1160 CTTTCCAGGCTTCCAGGACCTCTGATGGGAGAGCTGGGCGCCCTGAGCCACTGGGT 1219
DB 1224 CTTTCCAGGCTTCCAGGACCTCTGATGGGAGAGCTGGGCGCCCTGAGCCACTGGGT 1283
QY 1220 TGGAGTGGCCATGATCTCTGCTGGGCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT 1279
DB 1284 TGGAGTGGCCATGATCTCTGCTGGGCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT 1343
QY 1280 GTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT 1339
DB 1344 GTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT 1403
QY 1340 TCGAGGCTGAGGCTGATCTGACACCAACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1399
DB 1404 TCGAGGCTGAGGCTGATCTGACACCAACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1463
QY 1400 GAATTCCTTACCAAGTGCATGGAGAGAAATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1459
DB 1464 GAATTCCTTACCAAGTGCATGGAGAGAAATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1523
QY 1460 TAAATCAAGGAGCCATCAATTAATTTTATTTCTCTC 1499
DB 1524 TAAATCAAGGAGCCATCAATTAATTTTATTTCTCTC 1563

RESULT 13

US-10-201-853-245

; Sequence 245, Application US/10201853

; Publication No. US2004005335A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3430RLC465

; CURRENT FILING DATE: 2002-07-23

; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486

; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28

; Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 245

; LENGTH: 1564

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-201-853-245

Query Match 98.3%; Score 1473.6; DB 12; Length 1564;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1476; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 20 AGGTGTCGGGCTTTGCTGGCCAGCAAGCCTGATAGCATGAAGCTCTTATCTTTGGTGG 79

Db 84 AGGTGTCGGGCTTTGCTGGCCAGCAAGCCTGATAGCATGAAGCTCTTATCTTTGGTGG 143

Qy 80 CCGTGTGCGGCTTTGCTGGCCAGCAAGCCTGATAGCATGAAGCTCTTATCTTTGGTGG 139

Db 144 CTGTGTGCGGCTTTGCTGGCCAGCAAGCCTGATAGCATGAAGCTCTTATCTTTGGTGG 203

Qy 140 GGTGCAATGCACTCTGTCACCTTATAGAAACATCAGTGGGCAATATTTAGAACCAATG 199

Db 204 GGTGCAATGCACTCTGTCACCTTATAGAAACATCAGTGGGCAATATTTAGAACCAATG 263

220 TATCCCAAGAGGACTGCAACTGCTGCTGCAAGGTGGTGGAGCCCATGCCAATGCTGCTGGCCATG 259
264 TATCCCAAGAGGACTGCAACTGCTGCTGCAAGGTGGTGGAGCCCATGCCAATGCTGCTGGCCATG 323
260 ACCTGAGGGCCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 319
324 ACCTGAGGGCCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 383
320 TCAAGGTCACTCACTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 379
384 TCAAGGTCACTCACTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 443
390 TCCGTGATGCT 439
444 TCCGTGATGCT 503
440 ATGAGGAGGAGATGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 499
504 ATGAGGAGGAGATGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 563
520 CCGAGCAAAACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 559
564 CCGAGCAAAACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 623
560 TCGAG 619
624 TCGAG 683
620 GTGGTGGGTCAAGGCGCCCAACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 679
684 GTGGTGGGTCAAGGCGCCCAACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 743
680 GCTACTTCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT 739
744 GCTACTTCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT 803
740 CTTCTCCCTTACTTTAGAAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 799
804 CTTCTCCCTTACTTTAGAAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 863
800 TCTCTGATCTCTGTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 859
864 TCTCTGATCTCTGTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 923
860 GAAGGGAATGAGACATTCAGAGGCGGCTCAGGAGTGGATGGGATCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCT 919
924 GAAGGGAATGAGACATTCAGAGGCGGCTCAGGAGTGGATGGGATCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCT 983
920 CCACTCTTGCGGCTTCCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 979
984 CCACTCTTGCGGCTTCCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1043
980 CTGGGTCTTCAGGAACTCAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1039
1044 CTGGGTCTTCAGGAACTCAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1103
1040 CCTTCTGCACTGCTTCTTATCAGCACTCCCTCCAGCCCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1099
1104 CCTTCTGCACTGCTTCTTATCAGCACTCCCTCCAGCCCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1163
1100 CCACTCTTGCGGCTTCCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1159

Db 1164 CCAGCTCCAGCCCTGAGGACAGCTCTGATGGGAGAGCTGGGCCCTTGAGCCCACTGGGT 1223
Qy 1160 CTTTACGGGTGCATGGAAGCTGGTGTTCCTCTGCCCCGTGCACTTCTGCACCTGGGCA 1219
Db 1224 CTTTACGGGTGCATGGAAGCTGGTGTTCCTCTGCCCCGTGCACTTCTGCACCTGGGCA 1283
Qy 1220 TGGAGTGGCCATGCATCTACTCTGCTGCCGGTCCCTCACTGCACTTGGGGGTCTGGCA 1279
Db 1284 TGGAGTGGCCATGCATCTACTCTGCTGCCGGTCCCTCACTGCACTTGGGGGTCTGGCA 1343
Qy 1280 GTCCCTCTCTCCCAAGTCTCCACAGTCACTGAGCCAGAGGTGGTGGACATGAGAC 1339
Db 1344 GTCCCTCTCTCCCAAGTCTCCACAGTCACTGAGCCAGAGGTGGTGGACATGAGAC 1403
Qy 1340 TGGAGGCTGAGGTGGATCTGACACACAGCCCTGTACTTGGGTTCCTCTGTGTCCT 1399
Db 1404 TCGAGGCTGAGGTGGATCTGACACACAGCCCTGTACTTGGGTTCCTCTGTGTCCT 1463
Qy 1400 GAACTTCGTGTACCAAGTCCAGAGAGAAATTTGTCTCTGTCTAGAGTGTGTG 1459
Db 1464 GAACTTCGTGTACCAAGTCCAGAGAGAAATTTGTCTCTGTCTAGAGTGTGTG 1523
Qy 1460 TAAATCAGGAAGCCATCAATTAATTTCTTTCTCTC 1499
Db 1524 TAAATCAGGAAGCCATCAATTAATTTCTTTCTCTC 1563

RESULT 14

US-10-052-586-245
; Sequence 245, Application US/10052586
; Publication No. US20020127584A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/052,586
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063564
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; PRIOR APPLICATION NUMBER: 60/063734
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; PRIOR FILING DATE: 1997-11-13
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; PRIOR FILING DATE: 1997-11-24
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; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
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; PRIOR FILING DATE: 1998-04-21
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; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22

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| 7 | PRIOR APPLICATION NUMBER: 60/082719 | |
| 7 | PRIOR FILING DATE: 1998-04-22 | |
| 7 | PRIOR APPLICATION NUMBER: 60/083322 | |
| 7 | PRIOR FILING DATE: 1998-04-28 | |
| 7 | PRIOR APPLICATION NUMBER: 60/083495 | |
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| 7 | PRIOR APPLICATION NUMBER: 60/083496 | |
| 7 | PRIOR FILING DATE: 1998-04-29 | |
| 7 | PRIOR APPLICATION NUMBER: 60/083499 | |
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| 7 | PRIOR APPLICATION NUMBER: 60/083559 | |
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| 7 | PRIOR APPLICATION NUMBER: 60/084366 | |
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| 7 | PRIOR APPLICATION NUMBER: 60/084414 | |
| 7 | PRIOR FILING DATE: 1998-05-06 | |
| 7 | PRIOR APPLICATION NUMBER: 60/084639 | |
| 7 | PRIOR FILING DATE: 1998-05-07 | |
| 7 | PRIOR APPLICATION NUMBER: 60/084640 | |
| 7 | PRIOR FILING DATE: 1998-05-07 | |
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| 7 | PRIOR FILING DATE: 1998-05-07 | |
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| 7 | PRIOR APPLICATION NUMBER: 60/085580 | |
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| 7 | PRIOR APPLICATION NUMBER: 60/085700 | |
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| 7 | PRIOR APPLICATION NUMBER: 60/087268 | |
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| 7 | PRIOR APPLICATION NUMBER: 60/087609 | |
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| 7 | PRIOR APPLICATION NUMBER: 60/088167 | |
| 7 | PRIOR FILING DATE: 1998-06-05 | |
| 7 | PRIOR APPLICATION NUMBER: 60/088202 | |
| 7 | PRIOR FILING DATE: 1998-06-05 | |
| 7 | PRIOR APPLICATION NUMBER: 60/088212 | |
| 7 | PRIOR FILING DATE: 1998-06-05 | |
| 7 | PRIOR APPLICATION NUMBER: 60/088217 | |

Db 324 ACCTGGAGGCTACTGGCTGCTGTGGAGTGCAGTACGAGAGCGCAGACACACCA 383
Qy 320 TCAAGTCATCATTTGTCATCTACCTGTGGTGGTGGCTGTGTGTCTACATGGCT 379
Db 384 TCAAGTCATCATTTGTCATCTACCTGTGGTGGTGGCTGTGTGTCTACATGGCT 443
Qy 380 TCCGTATGCTGGTGGCTGTGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 439
Db 444 TCCGTATGCTGGTGGCTGTGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 503
Qy 440 ATGAGGAGGAGATGAGATGCTGGCTGTATGGCAGGAGTGTGTGTGTGTGTGTGT 499
Db 504 ATGAGGAGGAGATGAGATGCTGGCTGTATGGCAGGAGTGTGTGTGTGTGTGTGT 563
Qy 500 CCCGAGGAGGAGATGAGATGCTGGCTGTATGGCAGGAGTGTGTGTGTGTGTGTGT 559
Db 564 CCCGAGGAGGAGATGAGATGCTGGCTGTATGGCAGGAGTGTGTGTGTGTGTGTGT 623
Qy 560 TGCAGGAGGAGGAGATGAGATGCTGGCTGTATGGCAGGAGTGTGTGTGTGTGTGTGT 619
Db 624 TGCAGGAGGAGGAGATGAGATGCTGGCTGTATGGCAGGAGTGTGTGTGTGTGTGTGT 683
Qy 620 GTGGTGGGTCAAGGAGGAGGAGATGAGATGCTGGCTGTATGGCAGGAGTGTGTGTGT 679
Db 684 GTGGTGGGTCAAGGAGGAGGAGATGAGATGCTGGCTGTATGGCAGGAGTGTGTGTGT 743
Qy 680 GCTACTTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 739
Db 744 GCTACTTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 803
Qy 740 CTTCTCCCTTAAGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 799
Db 804 CTTCTCCCTTAAGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 863
Qy 800 TCTCTGATCTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 859
Db 864 TCTCTGATCTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 923
Qy 860 GAAGGAGATGAGACATTCGAGGCGGCTCAGAGTGGATGGATGCTGTCTCTCTGCT 919
Db 924 GAAGGAGATGAGACATTCGAGGCGGCTCAGAGTGGATGGATGCTGTCTCTCTGCT 983
Qy 920 CCACTCTTGGCGCTTCCAGCTCTGAGTCTTGGGATGTTGTTGTTGTTGTTGTTGTT 979
Db 984 CCACTCTTGGCGCTTCCAGCTCTGAGTCTTGGGATGTTGTTGTTGTTGTTGTTGTT 1043
Qy 980 CTGGGTCTTCAGGAACTCAGTGTCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1039
Db 1044 CTGGGTCTTCAGGAACTCAGTGTCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1103
Qy 1040 CTTTCTGAGTGTGTTTATCAGACCTCCCTCCAGCCGCTCAGGCTCAGGCTCAGGCT 1099
Db 1104 CTTTCTGAGTGTGTTTATCAGACCTCCCTCCAGCCGCTCAGGCTCAGGCTCAGGCT 1163
Qy 1100 CCAAGCTCCAGGCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1159
Db 1164 CCAAGCTCCAGGCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1223
Qy 1160 CTTCAAGGTCAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1219
Db 1224 CTTCAAGGTCAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1283
Qy 1220 TGGAGTGCCTATGCACTCTGCTGGCGGTCCCTCAGCTGCACTTGAAGGCTGTGGCA 1279

Db 1284 TGAAGTGGCCATGATCACTCTGCTGGCGGTCCCTCACTGCACTTGAAGGCTGTGGCA 1343
Qy 1280 GTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 1339
Db 1344 GTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 1403
Qy 1340 TGAAGCTGAGGCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1399
Db 1404 TGAAGCTGAGGCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1463
Qy 1400 GAAGCTGCTGTACAGGTCATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1459
Db 1464 GAAGCTGCTGT 1523
Qy 1460 TAAATCAAGGAGGATCACTTAAATTTGTTTATTTCTCTC 1499
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RESULT 15

US-10-174-590-245
; Sequence 245, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C42
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 245
; LENGTH: 1564
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-590-245

Query Match 98.3%; Score 1473.6; DB 14; Length 1564;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1476; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 20 AGTGTGTCCGGCTTTGCTGGCCAGCAAGCCTGATAGCATGAAGCTCTATCTTTGGTGG 79
Db 84 AGTGTGTCCGGCTTTGCTGGCCAGCAAGCCTGATAGCATGAAGCTCTATCTTTGGTGG 143
Qy 80 CCGTGTGGGTGTTTGTCTGGTGGCCCGCAGCTGAAGCCACAAAGAGTTCTGAAGATATCC 139
Db 144 CTGTGTGGGTGTTTGTCTGGTGGCCCGCAGCTGAAGCCACAAAGAGTTCTGAAGATATCC 203
Qy 140 GGTGAATGCACTGTCCACCTTATAGAAACATCAGTGGGCATATTTACACCAAGATG 199

[illegible]

Search completed: April 4, 2004, 00:36:12
Job time : 365.216 secs

OM nucleic - nucleic search, using sw model

Run on: April 3, 2004, 01:46:51 ; Search time 2536.04 Seconds
(without alignments)
17650.880 Million cell updates/sec

Title: US-10-030-269A-1
Perfect score: 1499
Sequence: 1 gcggctgcagcggctgtgta.....taaatgtttttattctctc 1499

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: em_esthum:**

3: em_estin:**

4: em_estnu:**

5: em_estov:**

6: em_estpl:**

7: em_estro:**

8: em_htc:**

9: gb_est1:**

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12: gb_est3:**

13: gb_est4:**

14: gb_est5:**

15: em_estfun:**

16: em_estom:**

17: em_gss_hum:**

18: em_gss_inv:**

19: em_gss_pin:**

20: em_gss_vrt:**

21: em_gss_fun:**

22: em_gss_man:**

23: em_gss_mus:**

24: em_gss_pro:**

25: em_gss_rod:**

26: em_gss_phg:**

27: em_gss_vrl:**

28: gb_gss1:**

29: gb_gss2:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| c 7 | 977.8 | 65.2 | 1201 | 13 | EX419772 | EX419772 EX419772 |
| c 8 | 963.6 | 64.3 | 1139 | 9 | AL515384 | AL515384 AL515384 |
| c 9 | 952.8 | 63.6 | 1201 | 9 | AL528644 | AL528644 AL528644 |
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| c 15 | 912 | 60.8 | 1201 | 13 | EX340039 | EX340039 EX340039 |
| c 16 | 911.6 | 60.8 | 1030 | 13 | EX394372 | EX394372 EX394372 |
| c 17 | 903.2 | 60.3 | 1201 | 13 | EX334437 | EX334437 EX334437 |
| c 18 | 901.2 | 60.1 | 1201 | 9 | AL514308 | AL514308 AL514308 |
| c 19 | 897.2 | 59.9 | 1017 | 13 | EX394373 | EX394373 EX394373 |
| c 20 | 896.8 | 59.8 | 1201 | 13 | EX341788 | EX341788 EX341788 |
| c 21 | 894.2 | 59.7 | 1201 | 9 | AL548272 | AL548272 AL548272 |
| c 22 | 890 | 59.4 | 977 | 13 | EX399479 | EX399479 EX399479 |
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| c 24 | 867.2 | 57.9 | 1124 | 13 | EX360008 | EX360008 EX360008 |
| c 25 | 851 | 56.8 | 1201 | 13 | EX393741 | EX393741 EX393741 |
| c 26 | 834 | 55.6 | 1201 | 13 | EX342010 | EX342010 EX342010 |
| c 27 | 833.6 | 55.6 | 893 | 9 | AL561955 | AL561955 AL561955 |
| c 28 | 831.2 | 55.5 | 881 | 9 | AL582044 | AL582044 AL582044 |
| c 29 | 831 | 55.4 | 934 | 9 | AL520688 | AL520688 AL520688 |
| c 30 | 830.4 | 55.4 | 908 | 13 | EX406848 | EX406848 EX406848 |
| c 31 | 829.6 | 55.3 | 923 | 9 | AL521080 | AL521080 AL521080 |
| c 32 | 829.4 | 55.3 | 907 | 13 | EX392869 | EX392869 EX392869 |
| c 33 | 824.8 | 55.0 | 914 | 13 | EX450777 | EX450777 AGENCOURT |
| c 34 | 811.6 | 54.1 | 933 | 13 | EX957082 | EX957082 AGENCOURT |
| c 35 | 808 | 53.9 | 1158 | 9 | AL516745 | AL516745 AL516745 |
| c 36 | 801.8 | 53.5 | 935 | 13 | EX948426 | EX948426 AGENCOURT |
| c 37 | 799.4 | 53.3 | 875 | 9 | AL560630 | AL560630 AL560630 |
| c 38 | 797.6 | 53.2 | 946 | 9 | AL520687 | AL520687 AL520687 |
| c 39 | 797.4 | 53.2 | 1159 | 13 | EX333999 | EX333999 EX333999 |
| c 40 | 789.4 | 52.7 | 1201 | 13 | EX342009 | EX342009 EX342009 |
| c 41 | 779.6 | 52.0 | 931 | 13 | EX41471 | EX41471 AGENCOURT |
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| c 43 | 769.8 | 51.4 | 944 | 13 | EX501879 | EX501879 AGENCOURT |
| c 44 | 767.8 | 51.2 | 868 | 14 | CD048308 | CD048308 AGENCOURT |
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ALIGNMENTS

RESULT 1
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LOCUS Homo sapiens HSPC186 mRNA, complete cds.
DEFINITION AF151020
ACCESSION AF151020
VERSION AF151020.1 GI:7106761
KEYWORDS HTC.

OM nucleic - nucleic search, using sw model

Run on: April 3, 2004, 00:09:01 ; Search time 4698.38 Seconds
(without alignments)
16863.481 Million cell updates/sec

Title: US-10-030-269A-3
Perfect score: 1828
Sequence: 1 aagcgacgacttcggccctc.....ctattttaagatcacatcagt 1828

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 3470272 seqs, 2167:516995 residues

Total number of hits satisfying chosen parameters: 6940544
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg: +
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8: gb_pl: +
9: gb_pr: +
10: gb_ro: +
11: gb_sts: +
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14: gb_vi: +
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Job time : 2552.24 secs

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 35: em_htg_r0d:**
 36: em_htg_mam:**
 37: em_htg_vrt:**
 38: em_sy:**
 39: em_htgo_hum:**
 40: em_htgo_mus:**
 41: em_htgo_other:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | | | DB | ID | Description |
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| 8 | 1499.4 | 82.0 | 217873 | 9 | HUAC004382 | Homo sapi | |
| c | 9 | 866 | 47.4 | 64365 | 2 | AC009089 | Homo sapi |
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| c | 12 | 453.2 | 24.8 | 474 | 6 | AX136667 | Sequence |
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| 14 | 391.4 | 21.4 | 1639 | 9 | BC054340 | Homo sapi | |
| 15 | 241.6 | 13.2 | 1717 | 10 | BC036386 | Mus muscu | |
| c | 16 | 133 | 7.3 | 235915 | 10 | AC129606 | Mus muscu |
| 17 | 131 | 7.2 | 194290 | 2 | AC137228 | Rattus no | |
| 18 | 131 | 7.2 | 194317 | 2 | AC137232 | Rattus no | |
| 19 | 131 | 7.2 | 256944 | 2 | AC096512 | Rattus no | |
| c | 20 | 72.4 | 4.0 | 191745 | 5 | AL929303 | Zebrafish |
| c | 21 | 63 | 3.4 | 161920 | 2 | AP002502 | Homo sapi |
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| c | 23 | 63 | 3.4 | 168922 | 9 | AP002007 | Homo sapi |
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| 29 | 60.8 | 3.3 | 165678 | 9 | AP002884 | Homo sapi | |
| c | 30 | 60.8 | 3.3 | 172859 | 2 | AC010815 | Homo sapi |
| c | 31 | 60.8 | 3.3 | 172930 | 2 | AC073305 | Homo sapi |
| c | 32 | 60.8 | 3.3 | 176485 | 9 | AP002841 | Homo sapi |
| c | 33 | 58.4 | 3.2 | 195637 | 2 | AP002420 | Homo sapi |
| c | 34 | 58.2 | 3.2 | 66623 | 2 | AC079057 | Homo sapi |
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| c | 37 | 58.2 | 3.2 | 167942 | 9 | AC021654 | Homo sapi |
| c | 38 | 57 | 3.1 | 157176 | 9 | AC007092 | Homo sapi |
| c | 39 | 57 | 3.1 | 201299 | 9 | AC007158 | Homo sapi |
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| 45 | 54.6 | 3.0 | 114540 | 9 | AC107426 | Homo sapi | |

ALIGNMENTS

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 VERSION AX136217.1 GI:14272625
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
 TITLE Secretory protein or membrane protein
 JOURNAL Patent: EP 1067182-A 139 10-JAN-2001;
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 Best Local Similarity 100.0%; Pred. No. 0;
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 QY 301 AGAGTCTTCTCACTTACACCCCCCAGGTATACAGACAGGGGCGGCGGAGGAGGAGGAGTACT 360

| | | | | | |
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| RESULT 2 | BD093295 | 1828 bp | DNA | linear | PAT 27-AUG-2002 |
| LOCUS | BD093295 | | | | |
| DEFINITION | Amyloid beta aglitation regulatory factor. | | | | |
| ACCESSION | ED093295 | | | | |
| VERSION | ED093295.1 | GI:22638683 | | | |
| KEYWORDS | WO 0104299-A/2. | | | | |
| SOURCE | Homo sapiens (human) | | | | |
| ORGANISM | Homo sapiens | | | | |
| REFERENCE | Eckaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. | | | | |
| AUTHORS | 1 (Bases 1 to 1828) Ota, I., Isogai, T., Nishikawa, T., Kawai, Y., Yamazaki, M., Sato, S., Arakawa, H. and Morita, M. | | | | |
| TITLE | Amyloid beta aglitation regulatory factor | | | | |
| JOURNAL | Patent: WO 0104299-A 2 18-JAN-2001; HELIX RESEARCH INSTITUTE, TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, YURI KAWAI, MAYAKO YAMAZAKI, SUSUMU SATO, HIROYUKI ARAKAWA, MASAHIKO MORITA | | | | |
| COMMENT | OS Homo sapiens (human) | | | | |
| | PN WO 0104299-A/2 | | | | |
| | 2D 18-JAN-2001 | | | | |

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| Q _y | 1141 | TTGCTGCTTTACTGAAATTTAACTGTTATTTGCTTCTCTCTCACTCCCAAGTGCACA | 1200 |
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PF 06-JUL-2000 WO 2000JP004515
PR 08-JUL-1999 JP 99P 194179,18-OCT-1999 US 60/159586 PI
TOSHIKO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, YURI KAWAI, MAYAKO PI
YAMAZAKI.
PI SUSUMU SATO, HIROXUKI ARAKAWA, YASAHIKO MORITA
PC C12N15/12, C07K14/47, C07K16/18, C12N5/10, A61K48/00, PC
A61K31/71,
PC A61P25/28, G01N33/15, G01N33/50
CC FH
CH CC
FT CDS

Location/Qualifiers
Key (83).. (487).

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
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QY 241 GCTTCCCAACTCATTTCTCAGCAGCATCTGAGCAGAGGGCGAGGAGGAGGAGCTA 360
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QY 781 AAAAAAGAAAACATACTGCCCTTCGAACTATGACAAAGCACTTCTGTGATCACTGAT 840
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QY 1021 GTTGTAGAGATCCTCCAGATAGCAAGATACCATCTCCAGAGACTGAGGGGATGACA 1080
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QY 1141 TTGCTGCTTTACTGAAATTAACGTGTTATTTCTGCTCTCTCATCTCCAGAGTGA 1200
DB 1141 TTGCTGCTTTACTGAAATTAACGTGTTATTTCTGCTCTCTCATCTCCAGAGTGA 1200
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 Db 1621 CTGGAGATTGACTGGTTCTTCCCTCAATAGGTTGGAATGGCTTATTTTGTGATA 1680
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 Db 1801 AAGAGCACTATTTTAAAGTACATCAGT 1828

RESULT 3
 BD123561 1828 bp DNA linear PAT 18-SEP-2002
 LOCUS
 DEFINITION Secretory protein or membrane protein.
 ACCESSION BD123561
 VERSION BD123561.1 GI:23218506
 KEYWORDS JP 2002017376-A/70.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1828)
 AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
 TITLE Secretory protein or membrane protein
 JOURNAL Patent: JP 2002017376-A 70 22-JUN-2002;
 COMMENT HELIX RESEARCH INSTITUTE
 OS Homo sapiens (human)
 PN JP 2002017376-A/70
 PD 22-JUN-2002
 PF 07-JUL-2000 JP 2002053173
 PI TOSHIO OTA,TAKAO ISOGAI,TEISUO NISHIKAWA,YURI KAWAI,TOMOYASU
 PI SUGIYAMA,
 PI KOJI HAYASHI
 PC 10,
 PC C12P21/02,C1201/68//C12P21/08,C12N15/00,C12N5/00 CC
 Secretory protein or membrane protein
 FH Key Location/Qualifiers
 FT CDS (83)..(487).
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Db 1 AAGCAGACGACTTCGGCCCTCCTTAGGGCCCTGGTCCGTAGCTACCGGTGCGGTCGCGCT 60
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 Db 61 GGGCGAGCTGCCCGCTTCCAAAATGGCGCGGGGGGGGTATCTGGTGGCTTGGCGGGG 120
 QY 121 GGGCTGGAGGCTCCTGCAGCTGGGATGCTGGCCGTGGCCGTGGCGACAGCCCTGGT 180
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 QY 181 GCGCGTGGCTTCCATGCTTCACTTGGGGCTAAGGTCTTCAATGATGACAGAGACGAC 240
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LOCUS AK075438 1828 bp mRNA linear PRI 03-SEP-2002

DEFINITION Homo sapiens cDNA PSEC0129 fls, clone PLACE1004170.
ACCESSION AK075438
VERSION AK075438.1 GI:22761526
KEYWORDS oligo capping; fls (full insert sequence).

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Kawai-Hio,Y., Hayashi,K.,
Ishii,S., Saito,K., Yamamoto,J., Wakamatsu,A., Nagai,T.,
Nakamura,Y., Nagahara,K., Sugano,S. and Isogai,T.

TITLE HRI human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1828)
AUTHORS Isogai,T. and Yamamoto,J.

TITLE Direct Submission
JOURNAL Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3996)

COMMENT HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass
sequencing, clone selection and full insert sequencing; Helix
Research Institute (supported by Japan Key Technology Center etc.);
cDNA library construction; Institute of Medical Science, University
of Tokyo, Laboratory of Genome Structure, Human Genome Center.

FEATURES
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ORIGIN
Query Match 100.0%; Score 1828; DB 9; Length 1828;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1828; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCGACGACTTCGCGCTCTTAGGGCGCTGCTCCGCTAGCTACCGGTGCGGTGCGGT 60
DB 1 AAGCGACGACTTCGCGCTCTTAGGGCGCTGCTCCGCTAGCTACCGGTGCGGTGCGGT 60

QY 61 GGGCGACGCTGCGCGCTTCGCAAAATGGCGGGCGGGGGATCTGGTGGCTTGGCGGGGC 120
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QY 1381 TTGCTTCTTAAAGTTTATGAGCAATATATGCTGCTAGGCTGTGCTAGTCCAGA 1440
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QY 1441 GACATGACAGGGGCTCAAAGTGGTCAAGATGGATCTGCTTCTGCGCTTGTGAGCTTCCA 1500
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QY 1501 GTCTAGCAACATTAATAAATAATACAAATGTTTACTTGAAGATGTGGTAAAGTCTAT 1560
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QY 1561 CAAAGAAAGTGTGTTGGGCTGTATATGAGGAGCCGATCATTAGATCAGTCAAG 1620
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QY 1681 TAAAGATTAATGAACATGGAATGGTCTTGAAGTGTGTTCTTAAAGGCACTTATGG 1740
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RESULT 4
AK075438

Search completed: April 3, 2024, 11:14:02
Job time : 4705.58 secs

Search completed: April 3, 2024, 11:14:02
Job time : 4705.58 secs

OM nucleic - nucleic search, using sw model

Run on: April 2, 2004, 21:47:00 ; Search time 457.958 Seconds
(without alignments)
16957.243 Million cell updates/sec

Title: US-10-C30-269A-3
Perfect score: 1828
Sequence: 1 aagcgacgacttcgcccctc.....ctattttaagcatcatcagt 1828

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseq1990s:*
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4: geneseq2001as:*
5: geneseq2001bs:*
6: geneseq2002s:*
7: geneseq2003as:*
8: geneseq2003bs:*
9: geneseq2003cs:*
10: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 1828 | 100.0 | 1828 | 4 AAF29358 | Aaf29358 Amyloid-b |
| 2 | 1828 | 100.0 | 1828 | 5 AAF93813 | Aaf93813 Human c1N |
| 3 | 1502.6 | 82.2 | 28149 | 5 ABA17961 | Abal7961 Human ner |
| 4 | 1499.4 | 82.0 | 10425 | 5 ABA17962 | Abal7962 Human ner |
| 5 | 1499.4 | 82.0 | 32192 | 5 ABA17963 | Abal7963 Human ner |
| 6 | 582.8 | 31.9 | 677 | 5 AAF94012 | Aaf94012 Primer sp |
| 7 | 457.4 | 25.0 | 1835 | 3 AAC76921 | Aac76921 Human ORF |
| 8 | 453.2 | 24.8 | 474 | 5 AAF94155 | Aaf94155 Primer sp |
| 9 | 432.4 | 23.7 | 1672 | 7 ABX63154 | Abx63154 Human c1N |
| 10 | 393.2 | 21.5 | 1652 | 4 AAS22866 | Aas22866 Human c1N |
| 11 | 391.4 | 21.4 | 1672 | 4 AAS22630 | Aas22630 Human c1N |
| 12 | 380.8 | 20.8 | 1290 | 6 ABK49891 | Abk49891 Human c1N |

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| 13 | 374.8 | 20.5 | 2692 | 5 | AAS73651 | Aas73651 DNA encod | |
| 14 | 372.8 | 20.4 | 1625 | 5 | AAS65051 | Aas65051 DNA encod | |
| 15 | 227.2 | 12.4 | 345 | 7 | ABX48511 | Abx48511 Bovire ES | |
| 16 | 206.2 | 11.3 | 486 | 8 | ACH14940 | Ach14940 Human adu | |
| 17 | 200 | 10.9 | 570 | 8 | ACH1441 | Ach1441 Human foe | |
| 18 | 171 | 9.4 | 465 | 4 | AAI15633 | Aai15633 Probe #55 | |
| 19 | 171 | 9.4 | 465 | 4 | ABA57650 | Aba57650 Human foe | |
| 20 | 171 | 9.4 | 465 | 4 | AAI37217 | Aai37217 Probe #59 | |
| 21 | 171 | 9.4 | 465 | 4 | ABA27068 | Aba27068 Probe #55 | |
| 22 | 171 | 9.4 | 465 | 4 | AAK31322 | Aak31322 Human bon | |
| 23 | 171 | 9.4 | 465 | 4 | AAK05704 | Aak05704 Human bra | |
| 24 | 171 | 9.4 | 465 | 4 | ABS31003 | Abs31003 Human liv | |
| 25 | 171 | 9.4 | 465 | 6 | ABS06074 | Abs06074 Human gen | |
| 26 | 165.8 | 9.1 | 169 | 4 | AAI24858 | Aai24858 Probe #14 | |
| 27 | 165.8 | 9.1 | 169 | 4 | ABA70272 | Aba70272 Human foe | |
| 28 | 165.8 | 9.1 | 169 | 4 | AAI50406 | Aai50406 Probe #19 | |
| 29 | 165.8 | 9.1 | 169 | 4 | ABA36985 | Aba36985 Probe #15 | |
| 30 | 165.8 | 9.1 | 169 | 4 | AAK44411 | Aak44411 Human bon | |
| 31 | 165.8 | 9.1 | 169 | 4 | AAK18498 | Aak18498 Human bra | |
| 32 | 165.8 | 9.1 | 169 | 4 | ABS44068 | Abs44068 Human liv | |
| 33 | 165.8 | 9.1 | 169 | 6 | ABS18646 | Abs18646 Human gen | |
| c | 34 | 117.4 | 6.4 | 904 | 5 | AAS65050 DNA encod | |
| 35 | 58.2 | 3.2 | 21082 | 5 | ABA17928 | Abal7928 Human ner | |
| 36 | 58.2 | 3.2 | 21087 | 5 | ABA17927 | Abal7927 Human ner | |
| c | 37 | 51.6 | 2.8 | 31129 | 6 | AAD36229 Human tra | |
| c | 38 | 51.2 | 2.8 | 1041 | 6 | ABS61503 Prostata | |
| 39 | 51 | 2.8 | 186591 | 7 | ACF62750 | Cancer ba | |
| 40 | 51 | 2.8 | 186591 | 7 | ADB20869 | NEP1 base | |
| 41 | 51 | 2.8 | 186591 | 9 | ADB87958 | Human UGT | |
| 42 | 51 | 2.8 | 186591 | 9 | ADB96941 | Human MDR | |
| 43 | 51 | 2.8 | 186591 | 9 | ADB92132 | Human MDR | |
| c | 44 | 51 | 2.8 | 208643 | 7 | ACF62735 | Cancer ba |
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ALIGNMENTS

RESULT 1
ID AAF29358 standard; DNA; 1828 BP.
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AC AAF29358;
XX
DT 20-APR-2001 (first entry)
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DE Amyloid-beta protein agglutination regulating factor DNA SEQ ID 3.
XX
KW Human; amyloid-beta protein; agglutination regulatory factor;
KW Alzheimer's disease; ds.
XX
OS Homo sapiens.
XX
PN W0200104299-Al.
XX
PD 18-JAN-2001.
XX
PF 06-JUL-2000; 2000WO-JP004515.
XX
PR 08-JUL-1999; 99JP-00194179.
PR 18-OCT-1999; 99US-0159586P.
XX
PA (HELI-) HELIX RES INST.

| | |
|-----|---|
| XX | Ota T, Isozai T, Nishikawa T, Kawai Y, Yamazaki M, Satoh S; |
| FFI | Arakawa H, Morita M; |
| XX | WPI; 2001-139347/14. |
| DR | |
| XX | |
| PPT | Polynucleotide encoding Amyloid-beta protein agglutination-controlling |
| PPT | factor, useful for inhibiting or promoting agglutination or sedimentation |
| PPT | of amyloid-beta protein and in diagnosis and screening drugs for |
| PPT | Alzheimer's disease. |
| XX | |
| PS | Claim 1; Page 46-48; 72pp; Japanese. |
| XX | |
| CC | This invention relates to polynucleotides AAF29357 - AAF29361 which |
| CC | encode proteins AAH49767 - AAH49771. The proteins inhibit or promote the |
| CC | agglutination of amyloid beta protein. The protein and polynucleotide |
| CC | sequences are useful in the diagnosis of Alzheimer's disease. They are |
| CC | also useful for screening drugs which are useful for treating Alzheimer's |
| CC | disease |
| XX | |
| SQ | Sequence 1828 BP; 497 Å; 409 C; 437 G; 485 T; 0 U; 0 Other; |
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| | Query Match 100.0%; Score 1828; DB 4; Length 1828; |
| | Best Local Similarity 100.0%; Pred. No. 0; |
| | Matches 1828; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
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| QY | 61 GGCGACGTGGCGCTTCCAAATGGCGCGCGCGCGGTATCTGTCGCTTGCGCGGCG 120 |
| DB | 61 GGCGACGTGGCGCTTCCAAATGGCGCGCGCGCGGTATCTGTCGCTTGCGCGGCG 120 |
| QY | 121 GGCGTGGAGGCTTCTCGAGCTGGCATGCGTSCCGGTGGCCCCGTTGGCGAAGAAGCCCTGT 180 |
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| QY | 181 GCCCGTGGCTTCACTGCTCAGTGTGGGCTTAAGGCTTTCAGTGAAGGAGGAGCA 240 |
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| QY | 241 GCCTCCCACACTATTCTCAGACAGATCTGACACAGAGGCGCGAAGAAAACCTGATCC 300 |
| DB | 241 GCCTCCCAACTATTCTCAGACAGATCTGACACAGAGGCGCGAAGAAAACCTGATCC 300 |
| QY | 301 AGAGTCTCTCATTCACCCGCCGATATACACAGAGGCGCGGAGGAGGAGGAGCA 360 |
| DB | 301 AGAGTCTCTCATTCACCCGCCGATATACACAGAGGCGCGGAGGAGGAGGAGCA 360 |
| QY | 361 TGAAAGTGAAGAGCATGTGACGACCGCATCTGACGGGAGCCCTGAGTTTGTGCCCCG 420 |
| DB | 361 TGAAAGTGAAGAGCATGTGACGACCGCATCTGACGGGAGCCCTGAGTTTGTGCCCCG 420 |
| QY | 421 CCACGGGTGGACACGAGGCGGATTCAGAAAGAGCCGAGGTGTGTATAGGTGAGGCTGG 480 |
| DB | 421 CCACGGGTGGACACGAGGCGGATTCAGAAAGAGCCGAGGTGTGTATAGGTGAGGCTGG 480 |
| QY | 481 GGCCACTCAACCAAGATGAGCCAGATGGAGTCAACCAAGGACGAGCGGGGGGCTCATG 540 |
| DB | 481 GGCCACTCAACCAAGATGAGCCAGATGGAGTCAACCAAGGACGAGCGGGGGGCTCATG 540 |
| QY | 541 CCTTCTCAAGTCTAAGCTCAGAAGCCCTCACAGCTGCGAAGTGAAGTGGTTTTTTCGCC 600 |
| DB | 541 CCTTCTCAAGTCTAAGCTCAGAAGCCCTCACAGCTGCGAAGTGAAGTGGTTTTTTCGCC 600 |

| | | | |
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| b | 541 | COITCTCOAGTCTAGCTCAGAGGCGGCTCAGAGCTGCAAGATTGACGTGGTGTITTTTTCOC | 600 |
| y | 601 | CAATAGGCTGGACTGGCTTTATTTTGTAGTTATAAAGAACATACCAATGGAGTGGTCT | 660 |
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| y | 661 | TGGAGTGTGTCTTAAGAGGCATCTATTAGGCGAAGATGTCTGTGATCAAACTCCCA | 720 |
| b | 661 | TGGAGTGTGTCTTAAGAGGCATCTATTAGGCGAAGATGTCTGTGATCAAACTCCCA | 720 |
| y | 721 | TGTTTCATTTGACTCTAGAGTCGCAATGGTGTAAAGAGCATCATTTTAAATGCATCAGT | 780 |
| b | 721 | TGTTTCATTTGACTCTAGAGTCGCAATGGTGTAAAGAGCATCATTTTAAATGCATCAGT | 780 |
| y | 781 | AAAAAGAAACATACCTGCGCTTCGAATCATGACAAAGCACTCTGTGATTCACTGAT | 840 |
| b | 781 | AAAAAGAAACATACCTGCGCTTCGAATCATGACAAAGCACTCTGTGATTCACTGAT | 840 |
| y | 841 | TTTTTAAATGAAAAATATACTGCATCTAGATTAAAGATGATGTGTGTTGAAAC | 900 |
| b | 841 | TTTTTAAATGAAAAATATACTGCATCTAGATTAAAGATGATGTGTGTTGAAAC | 900 |
| y | 901 | CCCAAGAGGCAACACTTTTGGAGCAACACACATCTTATTTCOCAGAACTCTAATAGCA | 960 |
| b | 901 | CCCAAGAGGCAACACTTTTGGAGCAACACACATCTTATTTCOCAGAACTCTAATAGCA | 960 |
| y | 961 | TTTTTCTGATTTAGTACAGACTGCTGCTTTAGATTAGGCAAGGCTCATGTTCCAGGCCAT | 1020 |
| b | 961 | TTTTTCTGATTTAGTACAGACTGCTGCTTTAGATTAGGCAAGGCTCATGTTCCAGGCCAT | 1020 |
| y | 1021 | GTTCGTAGAGATGCTCCAGCATAGCAAGTACCATCTCCAGAGACTGAGGGGATGACA | 1080 |
| b | 1021 | GTTCGTAGAGATGCTCCAGCATAGCAAGTACCATCTCCAGAGACTGAGGGGATGACA | 1080 |
| y | 1081 | GAGTTGCATCTTCATCCCAAGGCTTGTCTGCAAGGATCTACCCATGCAATGGGCAAG | 1140 |
| b | 1081 | GAGTTGCATCTTCATCCCAAGGCTTGTCTGCAAGGATCTACCCATGCAATGGGCAAG | 1140 |
| y | 1141 | TTCCTGCTTTACTGAAATTTAACTGTATTTCCTTTGCTTCTCTCACTCCCAAGTGCACA | 1200 |
| b | 1141 | TTCCTGCTTTACTGAAATTTAACTGTATTTCCTTTGCTTCTCTCACTCCCAAGTGCACA | 1200 |
| y | 1201 | TTTGTGTACAGAGTCTCATTTAGTAATGTGGTGTCTGCTGACTCCACTGTAGGCTCAAT | 1260 |
| b | 1201 | TTTGTGTACAGAGTCTCATTTAGTAATGTGGTGTCTGCTGACTCCACTGTAGGCTCAAT | 1260 |
| y | 1261 | GTGAAACTGACCATACAAACAAATATAAAAAAGATGTATGAAAAACCTATAATGACA | 1320 |
| b | 1261 | GTGAAACTGACCATACAAACAAATATAAAAAAGATGTATGAAAAACCTATAATGACA | 1320 |
| y | 1321 | CCAAAGATCATCTATCAACATTTATGCTTAGATCTTTCCAAATTAACCCCTTTATATGA | 1380 |
| b | 1321 | CCAAAGATCATCTATCAACATTTATGCTTAGATCTTTCCAAATTAACCCCTTTATATGA | 1380 |
| y | 1381 | TTCAATCTTTAAATGTTTATTGAGCAAAATATGTGCCTTAGGCACCTGTGCTAGTCCAGA | 1440 |
| b | 1381 | TTCAATCTTTAAATGTTTATTGAGCAAAATATGTGCCTTAGGCACCTGTGCTAGTCCAGA | 1440 |
| y | 1441 | GACATGACAGGGGTCAAAAGTGGTCAAGATGAGTCTGCTTCTGCCCTGTGTGAGCTTCCA | 1500 |
| b | 1441 | GACATGACAGGGGTCAAAAGTGGTCAAGATGAGTCTGCTTCTGCCCTGTGTGAGCTTCCA | 1500 |

QY 1501 GTCTAGCAACATTAAATAAATAATATACAAATGTTTACTTAGAAGATGTGTAAGTGTAT 1560
 DB |||||
 QY 1501 GTCTAGCAACATTAAATAAATAATATACAAATGTTTACTTAGAAGATGTGTAAGTGTAT 1560
 DB |||||
 QY 1561 CAGAGAAAGTGTGTTGGGCTGTATATGGAGGAGGAGCCGATCATTTAGATCAGGTACAG 1620
 DB |||||
 QY 1561 CAGAGAAAGTGTGTTGGGCTGTATATGGAGGAGGAGCCGATCATTTAGATCAGGTACAG 1620
 DB |||||
 QY 1621 CTGCGAGATTGACTGGTGTCTTTCCTCAATAGGTTGGAATGGCTTTATTTTGGATA 1680
 DB |||||
 QY 1621 CTGCGAGATTGACTGGTGTCTTTCCTCAATAGGTTGGAATGGCTTTATTTTGGATA 1680
 DB |||||
 QY 1681 TAAAGTAAATGAACCATGGATTTGGTCTTGAGAGTTGTCTTAAAGGCAACCTATGG 1740
 DB |||||
 QY 1681 TAAAGTAAATGAACCATGGATTTGGTCTTGAGAGTTGTCTTAAAGGCAACCTATGG 1740
 DB |||||
 QY 1741 CAGAGATTGTCTGTGATCAAACTACCATATTTCAATGACTCTTAAGATGCCATGGTGT 1800
 DB |||||
 QY 1741 CAGAGATTGTCTGTGATCAAACTACCATATTTCAATGACTCTTAAGATGCCATGGTGT 1800
 DB |||||
 QY 1801 AAGAGCACTATTTTAAAGTACATCAGT 1828
 DB |||||
 QY 1801 AAGAGCACTATTTTAAAGTACATCAGT 1828
 DB |||||

RESULT 2
 AAF93813
 ID AAF93813 standard; cDNA; 1828 BP.
 XX AAF93813;
 AC
 XX
 DT 23-MAY-2001 (first entry)
 XX
 XX Human cDNA encoding a membrane or secretory protein clone F5E0129.
 DE Human; secretory protein; membrane protein; vaccine; gene therapy;
 KW rheumatoid arthritis; diabetes; ss.
 OS Homo sapiens.
 XX
 XX EP1067182-A2.
 XX
 PD 10-JAN-2001.
 XX
 XX 07-JUL-2000; 2000EP-00114090.
 XX
 XX 08-JUL-1999; 99JP-00194179.
 PR 11-JAN-2000; 2000JP-00118775.
 PR 02-MAY-2000; 2000JP-00183766.
 XX
 XX (HELI-) HELIX RES INST.
 XX
 XX Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
 PI WPI; 2001-093989/11.
 DR P-PSDB; AAF93813.
 DR
 XX Nucleic acids encoding secretory proteins/membrane proteins, useful in
 PT gene therapy or as candidate target molecules in drug development.
 PT
 XX
 XX Claim 1; SEQ ID NO 139; 609pp + Sequence Listing; English.
 PS
 XX This invention relates to nucleic acid sequences AAF93744 - AAF93916
 CC

CC which encode human secretory or membrane proteins represented by AAF88317
 CC - AAF88419. Included in the invention are primers AAF93917 - AAF94295 and
 CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the
 CC invention. The invention also includes methods for the production of
 CC antibodies directed against the proteins, and cDNA sequences, which can
 CC be used in vaccines. The polynucleotide sequences and the proteins they encode may be
 CC therapy. The polynucleotide sequences and the proteins they encode may be
 CC used in the prevention, treatment and diagnosis of diseases associated
 CC with inappropriate secretory protein/membrane protein expression. The
 CC nucleic acids and complementary sequences may also be used as DNA probes
 CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
 CC and quantitate the presence of similar nucleic acid sequences in samples.
 CC They may also be used to study the expression and function of secretory
 CC proteins/membrane polypeptides and their role in metabolism. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC against them and in assays to identify modulators (agonists and
 CC antagonists) of expression and activity. The antibodies and antagonists
 CC may also be used as therapeutic agents to down regulate expression and
 CC activity. The antibodies may also be used as diagnostic agents for
 CC detecting the presence of the polypeptides in samples (e.g. by enzyme
 CC linked immunosorbent assay (ELISA). Examples of diseases which may be
 CC treated include rheumatoid arthritis and diabetes
 XX
 SQ Sequence 1828 BP; 497 A; 409 C; 437 G; 485 T; 0 U; 0 Other;

Query Match 100.0%; Score 1828; DB 5; Length 1828;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1828; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAGCAGACGACTTCGGCCCTCCTTAGGGCCGTGGTCCGTAGCTACCGGTGGCGGT 60
 DB 1 AAGCAGACGACTTCGGCCCTCCTTAGGGCCGTGGTCCGTAGCTACCGGTGGCGGT 60
 QY 61 GGGCGAGTGGCCGCTTCCAAATGGCGGCGCGCGGTATCTGGTGGTGGCGCGGC 120
 DB 61 GGGCGAGTGGCCGCTTCCAAATGGCGGCGCGCGGTATCTGGTGGTGGCGCGGC 120
 QY 121 GGGCTGGAGGCTCCTGCAGCTGGATGGCTGGCGGTGGCGGTGGCGGTGGT 180
 DB 121 GGGCTGGAGGCTCCTGCAGCTGGATGGCTGGCGGTGGCGGTGGCGGTGGT 180
 QY 181 GGGCGGTGGCTTCCATTCAGCTTGGGGGCTAAGGTCTTCAGATGAGCAGAGCACA 240
 DB 181 GGGCGGTGGCTTCCATTCAGCTTGGGGGCTAAGGTCTTCAGATGAGCAGAGCACA 240
 QY 241 GGGCGGTGGCTTCCATTCAGCTTGGGGGCTAAGGTCTTCAGATGAGCAGAGCACA 300
 DB 241 GGGCGGTGGCTTCCATTCAGCTTGGGGGCTAAGGTCTTCAGATGAGCAGAGCACA 300
 QY 301 GGGCGGTGGCTTCCATTCAGCTTGGGGGCTAAGGTCTTCAGATGAGCAGAGCACA 360
 DB 301 GGGCGGTGGCTTCCATTCAGCTTGGGGGCTAAGGTCTTCAGATGAGCAGAGCACA 360
 QY 361 GGGCGGTGGCTTCCATTCAGCTTGGGGGCTAAGGTCTTCAGATGAGCAGAGCACA 420
 DB 361 GGGCGGTGGCTTCCATTCAGCTTGGGGGCTAAGGTCTTCAGATGAGCAGAGCACA 420
 QY 421 GGGCGGTGGCTTCCATTCAGCTTGGGGGCTAAGGTCTTCAGATGAGCAGAGCACA 480
 DB 421 GGGCGGTGGCTTCCATTCAGCTTGGGGGCTAAGGTCTTCAGATGAGCAGAGCACA 480
 QY 481 GGGCGGTGGCTTCCATTCAGCTTGGGGGCTAAGGTCTTCAGATGAGCAGAGCACA 540
 DB 481 GGGCGGTGGCTTCCATTCAGCTTGGGGGCTAAGGTCTTCAGATGAGCAGAGCACA 540

Db 481 GGCCACTTAAACCAAGATGAGCCAGGATGGAGTCAACCGAGCGGGGGGCTCATG 540
QY 541 CTTCTTCCAGTCTAGCTCAGAGCCCTCAGAGTGAAGATGACTGGTTTTTTTCCOC 600
Db 541 CTTCTTCCAGTCTAGCTCAGAGCCCTCAGAGTGAAGATGACTGGTTTTTTTCCOC 600
QY 601 CAATAGGTGGACTGGCTTTATTTTGTAGTTATTAAGAACATACATGAGGTGGTTCT 660
Db 601 CAATAGGTGGACTGGCTTTATTTTGTAGTTATTAAGAACATACATGAGGTGGTTCT 660
QY 661 TGGGAGTTGTCTTAAGGCAATCTATTAGGCAAGATGCTGTGATCAAACTCCCA 720
Db 661 TGGGAGTTGTCTTAAGGCAATCTATTAGGCAAGATGCTGTGATCAAACTCCCA 720
QY 721 TGTTCATTGACTCTAAGATGCCATTTGTTTGAAGAGCATCATTTTAAATGATCAGT 780
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QY 781 AAAAAAGAAACATFACTGCCCTTCGAACHATGACAAAGCCCTTCTGTGATCAGCTGAT 840
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QY 841 TTTTAAATGAAMATATCTGCACTTAGATTAATGACATATGTTTGAAGAAC 900
Db 841 TTTTAAATGAAMATATCTGCACTTAGATTAATGACATATGTTTGAAGAAC 900
QY 901 CCCAAGAGGCAACACTTTGAGAGCAACACATCTTATTTCCAGAACTCTAATAGCA 960
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QY 1021 GTTGTAGAGATCTCCAGCATAGAGATACATCTCCAGAGACTGAGGAGATGACA 1080
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QY 1081 GAGTTGCATCTTCCATCCAGGCTTGCTGCAAGGCACTACCATGGCAATGGGCAAG 1140
Db 1081 GAGTTGCATCTTCCATCCAGGCTTGCTGCAAGGCACTACCATGGCAATGGGCAAG 1140
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QY 1381 TTTCATCTTTAAATGTTTATTGAGCAATTAATGTGCCCTAGGCACTGTGCTAGTCCAAGA 1440
Db 1381 TTTCATCTTTAAATGTTTATTGAGCAATTAATGTGCCCTAGGCACTGTGCTAGTCCAAGA 1440
QY 1441 GACATGAGGGGTCAAAAGTGGTCAAGATGGATCTGCTTCTGCTTGTGACCTTCCA 1500

Db 1441 GACATGAGGGGTCAAAAGTGGTCAAGATGGATCTGCTTCTGCTTGTGACCTTCCA 1500
QY 1501 GTCTAGCAACATTAATAAAAAATATAACAAATGTTTACTAGATGTGGTAAGTGTAT 1560
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Db 1741 CAAAGATTTGTCTGTGATCAAACTACCATATTTCAATGACTCTTAAGATGCCATTGGTGT 1800
QY 1801 AAGAGCACTATTTTAAAGTACATCAGT 1828
Db 1801 AAGAGCACTATTTTAAAGTACATCAGT 1828

Search completed: April 3, 2004, 03:01:53
Job time : 462.958 secs

Sequence 196, App
Sequence 1792, App
Sequence 13676, A
Sequence 2052, App
Sequence 165754, A
Sequence 28653, A
Sequence 292346, A
Sequence 5534, App
Sequence 23305, A
Sequence 3, Appl
Sequence 111, App
Sequence 112, App
Sequence 66, Appl
Sequence 94351, A
Sequence 318428, A
Sequence 17, Appl
Sequence 63792, A
Sequence 2, Appl
Sequence 3, Appl
Sequence 175, App
Sequence 93, Appl
Sequence 105, App
Sequence 2085, App
Sequence 45, Appl
Sequence 690, App
Sequence 220, App
Sequence 1716, App
Sequence 233933, A
Sequence 233934, A
Sequence 1, Appl
Sequence 1919, App
Sequence 93113, A
Sequence 93114, A
Sequence 93115, A
Sequence 242304, A
Sequence 46465, A
Sequence 46466, A
Sequence 2126, App
Sequence 588, App

5 391.4 21.4 1672 15 US-10-291-265-196
6 371.4 20.3 1649 14 US-10-102-524-1792
7 227.2 12.4 345 9 US-09-960-352-13676
8 206.2 11.3 486 10 US-09-918-993-2052
9 201.2 11.0 792 15 US-10-027-632-165754
10 200 10.9 570 15 US-09-918-993-28653
11 199.6 10.9 663 15 US-10-027-632-292346
12 171 9.4 465 9 US-09-864-761-5534
13 165.8 9.1 169 9 US-09-864-761-22305
14 51.6 2.8 3129 14 US-10-298-192-3
15 51.2 2.8 1041 14 US-10-000-256A-111
16 50.6 2.8 1380 14 US-10-000-256A-112
17 50.6 2.8 1654 9 US-09-764-864-66
18 48.2 2.6 341 15 US-10-027-632-94351
19 48.2 2.6 341 15 US-10-027-632-318428
20 47.4 2.6 56737 9 US-09-782-378A-17
21 47.2 2.6 579 15 US-10-027-632-83792
22 47.2 2.6 3673778 14 US-10-312-841-2
23 46.6 2.5 13737 11 US-09-900-448-3
24 46.6 2.5 6467 14 US-10-274-409-3
25 46.2 2.5 5908 12 US-10-221-613-175
26 46.2 2.5 5908 14 US-10-239-676-93
27 46.2 2.5 5908 14 US-10-240-453-105
28 46 2.5 7624 14 US-10-311-455-2085
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30 46 2.5 191395 12 US-10-235-192A-45
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35 45.6 2.5 1058 15 US-10-027-632-233934
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37 45 2.5 16611 14 US-10-311-455-1919
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41 44.2 2.4 611 15 US-10-027-632-242304
42 43.8 2.4 597 15 US-10-027-632-46465
43 43.8 2.4 597 15 US-10-027-632-46466
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45 43.4 2.4 13584 14 US-10-311-455-588

Search completed: April 4, 2004, 00:36:18
Job time : 445.276 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2004, 11:14:53 ; Search time 439.276 Seconds
(without alignments)
15564.412 Million cell updates/sec

Title: US-10-030-269A-3
Perfect score: 1828
Sequence: 1 aagcagacttcgcccctc.....ctattttaadcatcatcagt 1828

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2466186 seqs, 1870095128 residues

Total number of hits satisfying chosen parameters: 4932372

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:**

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:**
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- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query No. | Score | Match Length | ID | Description |
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| c | 1 | 723.8 | 39.6 | 733 15 | US-10-027-632-22239 Sequence 22239, A |
| | 2 | 628.6 | 34.4 | 629 15 | US-10-027-632-106372 Sequence 106372, A |
| | 3 | 432.4 | 23.7 | 1672 13 | US-10-044-C90-154 Sequence 154, App |
| | 4 | 393.2 | 21.5 | 1652 15 | US-10-291-265-668 Sequence 668, App |

OM nucleic - nucleic search, using sw model
Run on: April 3, 2004, 01:46:51 ; Search time 3092.65 Seconds
(without alignments)
17650.880 Million cell updates/sec

Title: US-10-030-269A-3
Perfect score: 1828
Sequence: 1 aagcgacgactccgcctc.....ctattttaagatcacatcagt 1828

Scoring table: IDENTITY_NUC
Gapop 10.0 ; Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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8: em_hic:*
9: gb_est1:*
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14: gb_est5:*
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16: em_estom:*
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18: em_gss_inr:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
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24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vri:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB | ID | Description |
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| 1 | 667 | 36.5 | 1123 | 10 | BF981721 | BF981721 602306073 |
| 2 | 620.4 | 33.9 | 657 | 14 | CK002119 | CK002119 AGENCOURT |
| 3 | 575 | 31.5 | 615 | 9 | AV734107 | AV734107 AV754107 |
| 4 | 414.4 | 22.7 | 1201 | 13 | BK420047 | BK420047 BK420047 |
| 5 | 412.4 | 22.6 | 666 | 12 | BG747410 | BG747410 602704895 |
| 6 | 406.4 | 22.2 | 751 | 12 | BE1762409 | BE1762409 603049088 |
| 7 | 405.8 | 22.2 | 513 | 10 | BE266566 | BE266566 601193557 |
| 8 | 405.6 | 22.2 | 692 | 14 | CD2444298 | CD2444298 AGENCOURT |
| 9 | 401.8 | 22.0 | 712 | 12 | BI596364 | BI596364 603243091 |
| 10 | 401.8 | 22.0 | 807 | 12 | BG723142 | BG723142 602693723 |
| 11 | 400.4 | 21.9 | 953 | 12 | BG754610 | BG754610 602714556 |
| 12 | 399.4 | 21.8 | 652 | 14 | CB108842 | CB108842 K-EST0149 |
| 13 | 398.4 | 21.6 | 766 | 12 | BG611096 | BG611096 602612045 |
| 14 | 397.2 | 21.7 | 950 | 9 | AL529270 | AL529270 AL529270 |
| 15 | 396.4 | 21.7 | 1329 | 10 | BF206117 | BF206117 601869474 |
| 16 | 395.4 | 21.6 | 788 | 12 | BI911876 | BI911876 603063693 |
| 17 | 395.4 | 21.6 | 808 | 12 | BI755131 | BI755131 603022850 |
| 18 | 394 | 21.6 | 596 | 9 | AV702496 | AV702496 AV702496 |
| 19 | 393.2 | 21.5 | 1201 | 9 | AL561086 | AL561086 AL561086 |
| 20 | 392.6 | 21.5 | 820 | 13 | BK443733 | BK443733 BK443733 |
| 21 | 392.4 | 21.5 | 490 | 12 | EM152926 | EM152926 TCBAPI013 |
| 22 | 391.4 | 21.4 | 517 | 14 | CB107125 | CB107125 K-EST0145 |
| 23 | 391.4 | 21.4 | 812 | 12 | BI759729 | BI759729 603045595 |
| 24 | 391.4 | 21.4 | 896 | 13 | BU509079 | BU509079 AGENCOURT |
| 25 | 391.4 | 21.4 | 1657 | 11 | BC029341 | BC029341 Homo sap1 |
| 26 | 389.8 | 21.3 | 795 | 10 | BE273072 | BE273072 601171379 |
| 27 | 389.4 | 21.3 | 768 | 12 | BG432592 | BG432592 602500752 |
| 28 | 388.6 | 21.3 | 495 | 12 | EM689573 | EM689573 UI-E-CK1- |
| 29 | 388.4 | 21.2 | 692 | 14 | CD671295 | CD671295 f902h05.y |
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| 31 | 388.4 | 21.2 | 1201 | 13 | EX422817 | EX422817 EX422817 |
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| 33 | 385 | 21.1 | 901 | 13 | EX421483 | EX421483 BX421483 |
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| 38 | 383.4 | 21.0 | 1033 | 12 | EM926195 | EM926195 AGENCOURT |
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| 42 | 381.2 | 20.9 | 1111 | 12 | EM921314 | EM921314 AGENCOURT |
| 43 | 381.2 | 20.9 | 1200 | 12 | EM906910 | EM906910 AGENCOURT |
| 44 | 380.6 | 20.8 | 911 | 13 | BU168294 | BU168294 AGENCOURT |
| 45 | 380.4 | 20.8 | 1002 | 12 | EM477319 | EM477319 AGENCOURT |

Search completed: April 3, 2004, 16:37:20
Job time : 3097.85 secs

ALIGNMENTS

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 DEFINITION
 AX136323
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS
 Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and
 Hayashi, K.
 TITLE
 JOURNAL
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 Patent: EP 1067182-A 245 10-JAN-2001;
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ORIGIN

Query Match 100.0%; Score 1584; DB 6; Length 1584;
 Best Local Similarity 100.0%; Pred. No. 1.1e-213;
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 VERSION WO C104299-A/3.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens

ORGANISM
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1584)
 Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Yamazaki,M., Sato,S.,
 Arakawa,H. and Morita,M.
 Amyloid beta agilation regulatory factor
 Patent: WO 0104299-A 3 18-JAN-2001;
 HELIX RESEARCH INSTITUTE,TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,
 YURI KAWAI,MAVAKO YAMAZAKI,SUSUMU SATO,HIROYUKI ARAKAWA, MASAHIKO
 MORITA

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

OS Homo sapiens (human)
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 PD 18-JAN-2001
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 Best Local Similarity 100.0%; Pred. No. 1.1e-213;
 Matches 1584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| | |
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| SOURCE | Homo sapiens (human) |
| ORGANISM | Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1584) |
| REFERENCE | Ora.T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K. |
| AUTHORS | Secretory protein or membrane protein |
| TITLE | Patent: JP 2002017376-A 123 22-JAN-2002; |
| JOURNAL | HELIX RESEARCH INSTITUTE |
| COMMENT | OS Homo sapiens (human) EN JP 2002017376-A/123 PD 22-JAN-2002 PF 07-JUL-2000 JP 2000253173 PI TOSHIO OTA,TAKAO ISOGAI,TEISUO NISHIKAWA,YURI KAWAI,TOMOYASU PI SUGIYAMA, PI KOJI HAYASHI PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC C12N1/21,C12N5/00 CC PC C12P21/02,C12Q1/68/C12P21/08,C12N15/30,C12N5/00 CC Secretory protein or membrane protein |
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| Qy | 61 TGGCCCCCTGCGCACCGCGGCGGGCGGTAGGGGGGTCAAGATGCTTGCGGCCCTTACCTCC 120 |
| Dd | 61 TCGCCCCCTGCGCACCGCGGCGGGCGGTAGGGGGGTCAAGATGCTTGCGGCCCTTACCTCC 120 |
| Qy | 121 CGGCTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180 |
| Dd | 121 CGGCTCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180 |
| Qy | 161 GCTGTGGGACGCCCCCTTGTTATGGACCTACACAGATCTGCAGAAGAGCAAGCGGGCTG 240 |
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| Qy | 241 GCCCGGCGGCGAGCGGAGTTGTGCAGGCTGAGCGGGAAGTGGTGGCAGAGCTAGCTCGG 300 |
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| Qy | 301 GSGCGCCCGCTCGGGGTGCAGAAATGCAAGTTCCAGTTCCGCTTCGCGCGCTGGAATTGC 360 |
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| Qy | 361 TCAGACACACAGAGCCCTTGGACGATCCTGCAACAGACAATTCGGAGAGCGGCTTC 420 |
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| QY | 421 | GTGTTCTGCACATGACTGGGGCCGGGCGACGCCAGCCGCGCTCAKCCGAGSSGCTGTCTATAGGCG | 480 |
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| QY | 481 | GACGCTGCTGCAGGTGCAGAGCGGCCCCGCTGGGGGCGCCCTCCCGGGGCGCTCGGCG | 540 |
| DB | 481 | GACGCTGCTGCAGGTGCAGAGCGGCCCCGCTGGGGGCGCCCTCCCGGGGCGCTCGGCG | 540 |
| QY | 541 | CTGGCTCGCGACCCCGGACGCCCTGGGCGCGGGGCTCCCGGGAAAGCGAGCGCGCTGG | 600 |
| DB | 541 | CTGGCGCGACCCCGGACGCCCTGGGCGCGGGGCTCCCGGGAAAGCGAGCGCGCTGG | 600 |
| QY | 601 | GACTGGGGAAGGCTGGGGGAGACGCTGGACTCTCGGGGAGCGAGCTCGAGGCTCTTTATG | 660 |
| DB | 601 | GAGTGGGGAAGGCTGGGGGAGACGCTGGACTCTCGGGGAGCGAGCTCGAGGCTCTTTATG | 660 |
| QY | 661 | GAGCGCGGACCAAGCGGGGACCGGAGACATCCCGCGGTTGGTGCACCTTGCACTGCAACAAC | 720 |
| DB | 661 | GAGCGCGGACCAAGCGGGGAGCGGAGACATCCCGCGGTTGGTGCACCTTGCACTGCAACAAC | 720 |
| QY | 721 | GAGCGCGGACGGCTGGCGGTGGGAGGCCACACGCGGACCGAGTTGCAAATCGCAAGCGCTG | 780 |
| DB | 721 | GAGGCGGACGGCTGGCGGTGGGAGGCCACACGCGGACCGAGTTGCAAATCGCAAGCGCTG | 780 |
| QY | 781 | TCGGGATCATTCGGGCTGGGACCTGCTGGCAGAGCTGGCTCCATTTGCGAGCTGGGCG | 840 |
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| QY | 841 | GCGCGGCTGCTGGAGCGCTTCACGCGGCGCTCACGCGCTCATGGGCAACAGCGCGCAAG | 900 |
| DB | 841 | GCGCGGCTGCTGGAGCGCTTCACGCGGCGCTCACGCGCTCATGGGCAACAGCGCGCAAG | 900 |
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| QY | 1201 | GCGCGCGCGCTAGACTGACTTCGCGCAGCGGTGGCTCGACCTGTGGGAGCTCAGGG | 1260 |
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| QY | 1261 | CACCGGCACCGGGGCTCTGGCGGTCSAGGCCACGCTCTCCTGCACAGGCGCACTC | 1320 |
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| QY | 1321 | CGAGGCTCTGGAAATGGTAGGCGAGGGGCTTAGAGGAGAGCGCCACCCACGAAAGGCC | 1380 |
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| SOURCE | |

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CDS

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Query Match 100.0%; Score 1584; DB 9; Length: 1584;
Best Local Similarity 100.0%; Pred. No. 1.1e-213;
Matches 1584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

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| QY | 841 | GGGGGGTGTGTGAGCGCTTCCACGCGGGCTCATGGCGCTCATGGCGACCAACGACGCGCAAG900 | |
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| DB | 901 | GGCCTGTGTGGCGGGCTCCGCGAGCTCAGAGCGCGGGCGGAGCGGAGCTCCTCTAGCGCC960 | |
| QY | 961 | GGCGATTGGCGCGAGTTCTGGCGCCGCCAACGACGCGAGCGGGCTCCCGCGGCGACGGGGT1020 | |
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| QY | 1021 | CGGGCTGCATATAGCAGGGCGCGGAGCTCAGGGGCTGGAGCTTGGTGTGTGGGGCGCG1080 | |
| DB | 1021 | CGGGCTGCATATAGCAGGGCGCGGAGCTCAGGGGCTGGAGCTTGGTGTGTGGGGCGCG1080 | |
| QY | 1081 | GGGCGACGCGCAGGAGGGTGGAGCTCGAGAGAGACTGGCTGTGGCGGTTCCACTGGTGG1140 | |
| DB | 1081 | GGGCGACGCGCAGGAGGGTGGAGCTCGAGAGAGACTGGCTGTGGCGGTTCCACTGGTGG1140 | |
| QY | 1141 | TGGGTAGTACAGTGGCAAGGCTGGCGTGTGGCGAGGAGCTCAGGCTCTGGCTGTGACCC1200 | |
| DB | 1141 | TGGGTAGTACAGTGGCAAGGCTGGCGTGTGGCGAGGAGCTCAGGCTCTGGCTGTGACCC1200 | |
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KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

1 Andrews, P., Walsh, J., and Gokhale, P.

AUTHORS Stem cell

TITLE Patent: WO 02077204-A 36 03-OCT-2002;

JOURNAL Aordia Limited (GB)

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| REFERENCE | 1 (bases 1 to 1702) |
| AUTHORS | Michael.R.B. and Tania.T.T. |
| TITLE | Wnt-6 polypeptide and Wnt-6 polynucleotide |
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 REFERENCE 1 (bases 1 to 1702)

AUTHORS Testa, T.T., Mossakowska, D.E., Carter, P.S., Hu, E., Zhu, Y.,
 Reisel, D.P., Murdoch, P.R., Herity, N.C., Lewis, C.J., Cross, D.A.,
 Culbert, A.A., Reith, A.D. and Barnes, M.R.
 TITLE Molecular cloning and characterization of six novel human WNT genes
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1702)
 AUTHORS Barnes, M.R.
 TITLE Direct Submission
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Job time : 4080.45 secs

OM nucleic - nucleic search, using sw model

Run on: April 2, 2004, 21:47:00 ; Search time 396.83 Seconds
(without alignments)
16957.243 Million cell updates/sec

Title: US-10-030-269A-5
Perfect score: 1584
Sequence: 1 ggcgtccgcgcgtccgact.....ataagattattaaaccacc 1584

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04.*

1: geneseqn1960s.*

2: geneseqn1990s.*

3: geneseqn2000s.*

4: geneseqn2001as.*

5: geneseqn2001bs.*

6: geneseqn2002s.*

7: geneseqn2003as.*

8: geneseqn2003bs.*

9: geneseqn2003cs.*

10: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|----------|--------------------|
| 1 | 1584 | 100.0 | 1584 | AAF29359 | Aaf29359 Amyloid-b |
| 2 | 1584 | 100.0 | 1584 | AAF93866 | Aaf93866 Human cDN |
| 3 | 1577.2 | 99.6 | 1726 | ABX75316 | Abx75316 Human cDN |
| 4 | 1577.2 | 99.6 | 1726 | AAD52541 | Aad52541 WNT-6 DNA |
| 5 | 1577.2 | 99.6 | 1726 | ABZ81813 | Abz81813 Ligand WN |
| 6 | 1573.2 | 99.3 | 1702 | AAZ91783 | Aaz91783 Human Wnt |
| 7 | 1434.4 | 90.6 | 1754 | ACC51101 | Acc51101 Human Sol |
| 8 | 1434.4 | 90.6 | 1754 | ACC51102 | Acc51102 Human Sol |
| 9 | 1333.8 | 84.2 | 1855 | ACC51108 | Acc51108 Human Sol |
| 10 | 848.2 | 53.5 | 959 | ADD78265 | Add78265 Human CGD |
| 11 | 520 | 32.8 | 526 | AAF94068 | Aaf94068 Primer sp |
| 12 | 512 | 32.3 | 512 | ABS70488 | Abs70488 Human bon |
| 13 | 466.6 | 29.5 | 803 | AAD16763 | Aad16763 Human nov |

| | | | | | | |
|----|-------|------|------|---|-----------|---------------------|
| 14 | 466.6 | 29.5 | 803 | 9 | ADC22055 | Adc22055 Human cDN |
| 15 | 322 | 20.3 | 342 | 7 | AEE236692 | Aee236692 Human GEN |
| 16 | 213.2 | 13.5 | 1202 | 4 | AAD16767 | Aad16767 Human nov |
| 17 | 213.2 | 13.5 | 1202 | 9 | ADC22059 | Adc22059 Human cDN |
| 18 | 213.2 | 13.5 | 1228 | 3 | AAZ290451 | Aaz290451 Wnt-4AF a |
| 19 | 213.2 | 13.5 | 1515 | 7 | ABX62938 | Abx62938 Human act |
| 20 | 213.2 | 13.5 | 1515 | 4 | AAI58045 | Aai58045 Human pol |
| 21 | 211.6 | 13.4 | 1598 | 4 | AAI59831 | Aai59831 Human pol |
| 22 | 211.6 | 13.4 | 2049 | 2 | AAZ34081 | Aaz34081 Human PRO |
| 23 | 211.6 | 13.4 | 2049 | 3 | AAZ78505 | Aaz78505 Human PRO |
| 24 | 211.6 | 13.4 | 2049 | 4 | AAZ45964 | Aaz45964 Human DNA |
| 25 | 211.6 | 13.4 | 2049 | 7 | ABX78567 | Abx78567 Human PRO |
| 26 | 211.6 | 13.4 | 2049 | 7 | ACA75539 | Aca75539 Novel hum |
| 27 | 211.6 | 13.4 | 2049 | 7 | ACA71019 | Aca71019 Human sec |
| 28 | 211.6 | 13.4 | 2049 | 7 | ACC87547 | Acc87547 Human sec |
| 29 | 211.6 | 13.4 | 2049 | 7 | ACC86933 | Acc86933 Human sec |
| 30 | 211.6 | 13.4 | 2049 | 7 | ACD04106 | AcD04106 Human sec |
| 31 | 211.6 | 13.4 | 2049 | 7 | ACA9437 | AcA9437 cDNA enco |
| 32 | 211.6 | 13.4 | 2049 | 7 | ACA90282 | AcA90282 Novel hum |
| 33 | 211.6 | 13.4 | 2049 | 7 | ACC89389 | Acc89389 Human sec |
| 34 | 211.6 | 13.4 | 2049 | 7 | ACA98180 | AcA98180 Novel hum |
| 35 | 211.6 | 13.4 | 2049 | 7 | ACA93822 | AcA93822 Human sec |
| 36 | 211.6 | 13.4 | 2049 | 7 | ACD15215 | AcD15215 Human sec |
| 37 | 211.6 | 13.4 | 2049 | 7 | ACD08802 | AcD08802 Human sec |
| 38 | 211.6 | 13.4 | 2049 | 7 | ACC96722 | Acc96722 Human sec |
| 39 | 211.6 | 13.4 | 2049 | 7 | ACF15443 | AcF15443 Human sec |
| 40 | 211.6 | 13.4 | 2049 | 7 | ACD42614 | AcD42614 Novel hum |
| 41 | 211.6 | 13.4 | 2049 | 7 | ACA72910 | AcA72910 Human PRO |
| 42 | 211.6 | 13.4 | 2049 | 7 | ACD02982 | AcD02982 Novel hum |
| 43 | 211.6 | 13.4 | 2049 | 7 | ACD01797 | AcD01797 Novel hum |
| 44 | 211.6 | 13.4 | 2049 | 7 | ACA91989 | AcA91989 Novel hum |
| 45 | 211.6 | 13.4 | 2049 | 7 | ACA63649 | AcA63649 Novel hum |

ALIGNMENTS

RESULT 1

AAF29359

ID AAF29359 standard; DNA; 1584 BP.

XX

AC AAF29359;

XX

DT 20-APR-2001 (first entry)

XX

DE Amyloid-beta protein agglutination regulating factor DNA SEQ ID 5.

XX

KW Human; amyloid-beta protein; agglutination regulatory factor;

XX

KW Alzheimer's disease; ds.

XX

OS Homo sapiens.

XX

PN WO200104259-A1.

XX

PD 18-JAN-2001.

XX

PF 06-JUL-2000; 2000WO-JP004515.

XX

PR 08-JUL-1999; 99JP-00194179.

XX

PR 18-OCT-1999; 99US-0159566P.

XX

PA (HELI-) HELIX RES INST.

XX

CC and (iii) nucleic acid molecules which are degenerate as a result of the
CC genetic code to the sequences of (i) or (ii); (b) forming a culture
CC comprising the cell identified in (a) with an embryonic stem cell; and
CC (c) growing the culture for the maintenance of embryonic stem cells in an
CC undifferentiated state; and (4) A cell, therapeutic cell or cell culture
CC obtainable by any of the methods cited above. The therapeutic cell of the
CC present invention is useful in the treatment of an animal, preferably a
CC human, comprising administering a cell composition comprising embryonic
CC stem cells which have been induced to differentiate into at least one
CC cell-type. The cell is also useful for the manufacture of a composition
CC for use in treatment of diseases such as Parkinson's disease,
CC Huntington's disease, motor neuron disease, heart disease, diabetes,
CC liver disease (e.g. cirrhosis), renal disease and AIDS (acquired
CC immunodeficiency syndrome). The present sequence encodes a Wnt or
CC Notch pathway protein (i.e. a ligand for the method of the invention)
XX
SQ Sequence 1726 BP; 274 A; 631 C; 570 G; 251 T; 0 U; 0 Other;

Query Match 99.6%; Score 1577.2; DB 7; Length 1726;
Best Local Similarity 99.8%; Pred. No. 3.9e-276;
Matches 1579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGCCTCGCGGCGCTCGCACTGAGAGCCGGGGGCGCTCGGGCGCGGGTTCCGCCCGCAGCC 60
DB 125 GGCCTCGCGGCGCTCGCACTGAGAGCCGGGGGCGCTCGGGCGCGGGTTCCGCCCGCAGCC 184
QY 61 TCGCCCTCCCTCGCCACCCGGGGCGCGCTAGGGCGGTACGATGCTCGCGCCCTTACCCCTCC 120
DB 185 TCGCCCTCCCTCGCCACCCGGGGCGCGCTAGGGCGGTACGATGCTCGCGCCCTTACCCCTCC 244
QY 121 CGCCTCGGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 245 CGCCTCGGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 304
QY 181 GCTGTGGGCGACCGCCCTTGCTTATGACCGCTTACGACATCTGACGAGAGGCAAGCGGGCTG 240
DB 305 GCTGTGGGCGACCGCCCTTGCTTATGACCGCTTACGACATCTGACGAGAGGCAAGCGGGCTG 364
QY 241 GCGGGGCGGCGAGCGCGAGTGTGCGAGGCTGAGCGCGAGAGTGTGCGAGAGCTAGCTCGG 300
DB 365 GCGGGGCGGCGAGCGCGAGTGTGCGAGGCTGAGCGCGAGAGTGTGCGAGAGCTAGCTCGG 424
QY 301 GCGCGCGCGCTCGGGGTGCGAGAGTGTGCGAGTGTGCGAGTGTGCGAGTGTGCGAGTGTGCG 360
DB 425 GCGCGCGCGCTCGGGGTGCGAGAGTGTGCGAGTGTGCGAGTGTGCGAGTGTGCGAGTGTGCG 484
QY 361 TCCAGCGCCACAGAGGCGCTTTGAGCGCATCTCTGCAACAGGACATTCGGGAGAGCGGCTTC 420
DB 485 TCCAGCGCCACAGAGGCGCTTTGAGCGCATCTCTGCAACAGGACATTCGGGAGAGCGGCTTC 544
QY 421 GTGTTGCGCATCACTGCGGGCGGGCGCGAGCGCGCGCTGACGCGAGCGCTGTCTATGGGC 480
DB 545 GTGTTGCGCATCACTGCGGGCGGGCGCGAGCGCGCGCTGACGCGAGCGCTGTCTATGGGC 604
QY 481 GAGCT 540
DB 605 GAGCT 664
QY 541 CTGCCCGGCAACCCCGGAGCCCTTGGCGCGCGCGGGCTCCCGGAGGAGCGAGCGCGCGCTGG 600
DB 665 CTGCCCGGCAACCCCGGAGCCCTTGGCGCGCGCGGGCTCCCGGAGGAGCGAGCGCGCGCTGG 724
QY 601 GAGTGGGGAGGCTGCGGGCGAGGACCTGGACTTCGGGGGAGGAGAGTGGAGGCTCTTTATG 660

DB 725 GAGTGGGGAGGCTGCGGGGAGACAGCTGGAGCTTGGGGGAGGAGAGTGGAGGCTCTTTATG 784
QY 661 GACGCGCGGCGACAGCGGGGAGCCCGGAGCATCCCGGGGCTTGGTGAACCTGCAACAAC 720
DB 785 GACGCGCGGCGACAGCGGGGAGCGGAGCATCCCGGGGCTTGGTGAACCTGCAACAAC 844
QY 721 GAGCGGCGGAGGCTGGCGGTGCGGAGCGGAGCGGAGCATCCCGGGGCTTGGTGAACCTGCAACAAC 780
DB 845 GAGCGGCGGAGGCTGGCGGTGCGGAGCGGAGCGGAGCATCCCGGGGCTTGGTGAACCTGCAACAAC 904
QY 781 TCGGATCATGCGGCGCTCGGAGCATCTGCTGCGAGAGCTGCGCTTCCGAGGCTGGGC 840
DB 905 TCGGATCATGCGGCGCTCGGAGCATCTGCTGCGAGAGCTGCGCTTCCGAGGCTGGGC 964
QY 841 GCGCGGCTGCTGGAGGCTTCCAGCGGCGCTCAGCGGCTCATGGGCAACAGCGGCAAG 900
DB 965 GCGCGGCTGCTGGAGGCTTCCAGCGGCTCAGCGGCTCATGGGCAACAGCGGCAAG 1024
QY 901 GCGCTGCTGGCGCGGTCCGAGCGCTCAAGCGCGCGGGCGGAGCGGAGCTCTCTAGGCG 960
DB 1025 GCGCTGCTGGCGCGGTCCGAGCGCTCAAGCGCGCGGGCGGAGCGGAGCTCTCTCTAGGCG 1084
QY 961 GCGGATTCGCGCGCTTCTGCGCGCCCGCAACCGAGCGACCGGGCTCCCGCGGCGAGCGGGGT 1020
DB 1085 GCGGATTCGCGCGCTTCTGCGCGCCCGCAACCGAGCGACCGGGCTCCCGCGGCGAGCGGGGT 1144
QY 1021 CGCGGCTGCATAGCAGCGCGCGGAGCTCTGAGCGGCTGCGACCTGCTGCTGCTGCGGGCGCG 1080
DB 1145 CGCGGCTGCATAGCAGCGCGCGGAGCTCTGAGCGGCTGCGACCTGCTGCTGCTGCGGGCGCG 1204
QY 1081 GCGGACCGGCGAGAGGCTGCGAGCTCGAGAGAGCTGCGCTGCTGCGGCTTCCAGCTGGTGC 1140
DB 1205 GCGGACCGGCGAGAGGCTGCGAGCTCGAGCTCGAGAGAGCTGCGCTGCTGCGGCTTCCAGCTGGTGC 1264
QY 1141 TCGGTAGTACAGTCCCAACCGCTGCGGTGTGCGGAGAGAGCTCAAGCTCTGCTGCTGAGCG 1200
DB 1265 TCGGTAGTACAGTCCCAACCGCTGCGGTGTGCGGAGAGAGCTCAAGCTCTGCTGCTGAGCG 1324
QY 1201 GCGGCGCGGCGCTGAGCTGAGCTTGGCGAGCGGCTGCGTCAAGCTGTGGGAGCTCAGGG 1260
DB 1325 GCGGCGCGGCGCTGAGCTGAGCTTGGCGAGCGGCTGCGTCAAGCTGTGGGAGCTCAGGG 1384
QY 1261 CACGGGCGAGCGGGGCGCTCTCGCGCTCGAGCGCGAGCTCTCCCTGCGGAGAGCGGAGCTC 1320
DB 1385 CACGGGCGAGCGGGGCGCTCTCGCGCTCGAGCGCGAGCTCTCCCTGCGGAGAGCGGAGCTC 1444
QY 1321 CCAAGGCTCTGGAATGCTGAGCGCGGAGGCTTGGAGAGAGCGGAGCGGAGCGGAGCGGAG 1380
DB 1445 CCAAGGCTCTGGAATGCTGAGCGCGGAGGCTTGGAGAGAGCGGAGCGGAGCGGAGCGGAG 1504
QY 1381 AGGGGCGAGAGCGGGCGCGGAGGCTTGGAGAGAGCGGAGCTTAAAGGAGAGCTGTACAGGCG 1440
DB 1505 AGGGGCGAGAGCGGGCGCGGAGGCTTGGAGAGAGCGGAGCTTAAAGGAGAGCTGTACAGGCG 1564
QY 1441 CTCCCTCCCGCTTGGGCTCTAGGAGAGAGAGCTTTTAAAGGAGAGCTTAAAGGAGAGCTGTACAGGCG 1500
DB 1565 CTCCCTCCCGCTTGGGCTCTAGGAGAGAGAGCTTTTAAAGGAGAGCTTAAAGGAGAGCTGTACAGGCG 1624
QY 1501 AGGCGCTCTGGATCTAGGCGCTCCCGAGAGCTGCTGCGGAGAGAGCTGCTGGGTGAGGCTT 1560
DB 1625 AGGCGCTCTGGATCTAGGCGCTCCCGAGAGCTGCTGCGGAGAGAGCTGCTGGGTGAGGCTT 1684

QY 1561 ATCAATAAGATATTTAACCA 1582
 |||||

DB 1685 ATCAATAAGATATTTAACCA 1706

RESULT 4
AAD52541
ID AAD52541 standard: DNA: 1726 BP:

| | |
|----|---------------------------|
| AK | |
| AC | AAD52541; |
| XX | |
| DT | 02-MAY-2003 (first entry) |

DE WNT-6 DNA.

| | | |
|----|---------------|------------------|
| XX | Unidentified. | Location/Qualifi |
| OS | | |
| XX | | |
| FH | Key | |

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E1  CDS
E2  /tag= a
E3  /product= "WNT-6"
E4  /note= "this CDS
E5

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F1
 XX
 PN
 YY

WO20029092-A2.

use reading

FD 14-NCV-2002.
XX
PF 29-APR-2002; 2002WO-GB001946.
YY

04-PAI-200-7 2001GS-00011004.
(AXOR-) AXORDIA LTD.

PI Andrews P, Draper J, Walsh J;
XX
DR WPI; 2003-120579/11.

XX Identifying biologically active
PT cells into a cell array, exposing
PT

PT exposure to the agent.
XX
PS Claim 19; Fig 36; 90pp; English..

CC The present invention relates to
CC the identification of biological
CC effect through the activation of

CC reporter molecule, cloning the
CC exposing the array to at least
CC signal generated by the reporter

CC the genes through which the agent
CC their ability to activate certain
CC assay, in identifying relationships

CC differentiation of embryonic stem
CC testing for unwanted activation
CC pathways. The present sequence is

CC of the invention
XX
SQ Sequence 1726 BP; 274 A; 631 C; 570 G; 251 T; 0 U; 0 Other;

| | | | | |
|----------------------------|--------|---------------------|-------|-------------------|
| Query Match | 99.6%; | Score 1577.2; | DB 7; | Length 1726; |
| Best Local Similarity | 99.8%; | Pred. No. 3.9e-276; | | |
| Matches 1579; Conservative | 0; | Mismatches | 3; | Indels 0; Gaps 0; |

Qy

1 GGGCTCGGCGGCGACTCGGACTGAAGCCCGGGGCCCTCGGCGGCGCGGTTCGCCCGCGCAGGC 60
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Db

125 GGGCTCGGCGGCGACTGAAGCCCGGGGCCCTCGGCGGCGCGGTTCGCCCGCGCAGGC 184

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|-----|---|-----|
| 61 | TGGGCCCCCTGCCACCCGGGGGGCGGTAGGGCGGTCAAGTACTGTCGGCCCTTACCCCTCC | 120 |
| | | |
| 135 | TGGGCCCCCTGCCACCCGGGGGGCGGTAGGGCGGTCAAGTACTGTCGGCCCTTACCCCTCC | 244 |
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Qy 121 CGGCTCGGGCTGCTGCTGCTGCTGCTGTGGCCGCCGACGTGGCGGACCTGTGGTGG 180
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D6 245 CGGCTCGGGCTGCTGCTGCTGCTGCTGCTGTGGCCGCCGACGTGGCGGACCTGTGGTGG 304
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181 GCTGTGGGAGCCCCCTTGGTTATGGACCCTTACCAGCATCTTGCAAGAAAGGACGGGGCTG 240
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305 GCTGTGGGAGCCCCCTTGGTTATGGACCCTTACCAGCATCTTGCAAGAAAGGACGGGGGGCTG 364

Qy 241 GCCGGCGGCGAGGCCGAGTGTTCACAGGCCTGAGCCGGAAATGGTGCAAGAATCCTCGG 300
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|||||
D6 365 GCCGGCGGCGAGGCCGAGTGTTCACAGGCCTGAGCCGGAAATGGTGCAAGAATCCTCGG 424
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Qy 301 GGCGCCGGCTCGGGTTCGAGAGTGCCAGTGCCAGTTCGCTTCGCGCGTGGAAATTGC 360
|||||
Dd 425 GGCGCCGGCTCGGGTTCGAGAGTGCCAGTGCCAGTTCGCTTCGCGCGTGGAAATTGC 484
|||||

361. TCACGCCACAGCAAGGCTTTGGACGGCATCCTGCAACAGGACATTCGGGGACACGGGCTTC 420

Qy

485 TCACGCCACAGCAAGGCTTTGGACGGCATCCTGCAACAGGACATTCGGGGACACGGGCTTC 544

Db

421 GTGTTGGCATCACTGGGCGGGGCGAGCAACCAAGCCGCTACACAGGCGCTGTTCTATGGGC 480

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545 GTGTTGGCATCACTGGGCGGGGCGAGCAACCAAGCCGCTACACAGGCGCTGTTCTATGGGC 604

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QY 481 GAGTGTGCAGTGCAGTGCAGGCGCCCGCTGGGGGGCCCTCCCGGCGCTCGGC 540
|||||
D6 605 GAGTGTGCAGTGCAGTGCAGGCGCCCGGGGGCGCCCTCCCGGCGCTCGGC 664

QY 541 CTGCTCGGCACTCCCGGACCCCTGGCCCGGGGCTCCCGGAGGCAAGCGCGCTGG 600
|||||
nb 665 CTGCTCGGCACTCCCGGACCCCTGGCCCGGGGCTCCCGGAGGCAAGCGCGCTGG 724

Q7 601 GAGTGGGAGGCTCGGGCGAAGACCTGGACTTCGGGACGAGAGTCGAGGCTCTTATG 660
|||||
725 GAGTGGGAGGCTTCGGCGACGAGCTGACCTTCGGGACGAGAGTCGAGGCTCTTATG 784

Qy 661 GACGCGGACAAAGGGGACCGGGAGACATCCGCGGTTGGTGAACTGGACACAC 720

[illegible]

Qy 781 TCGGATCATGCGGCTGGCACTGCTGGCGAAGCTGCTCCATTGGCGAGGTGGGC 840

Qk 905 TCGGATCATGCGGCTGGCACTGCTGGCGAAGCTGCTCCATTGGCGAGGTGGGC 964

| | |
|----|---|
| XX | Ligand; WNT-5A; stem cell; stem-loop RNA; antianaemic; cerebroprotective; |
| XX | neuroprotective; nootropic; antiparkinsonian; cardiatic; hepatotropic; |
| XX | anticancer; vulnary; gene therapy; gene; ds. |
| XX | Unidentified. |
| XX | WO2003012082-A2. |
| XX | 13-FEB-2003. |
| XX | 25-JUL-2002; 2002WO-GB003409. |
| XX | 26-JUL-2001; 2001GB-00018223. |
| XX | (AXOR-) AXORDIA LTD. |
| XX | Andrews P, Walsh J, Gokhale P; |
| XX | WFI; 2003-276398/27. |
| XX | Modulating the differentiation state of a stem cell, useful for treating |
| XX | e.g. pernicious anemia, stroke, cirrhosis, diabetes or a |
| XX | neurodegenerative disease, comprises contacting a stem cell with a stem |
| XX | loop RNA. |
| XX | Claim 7; Fig 23; 85pp; English. |
| XX | The present sequence is the nucleic acid sequence of ligand WNT-5A. The |
| XX | invention relates to a method of modulating the differentiation state of |
| XX | a stem cell, such as an embryonic stem cell, embryonic germ cell, |
| XX | embryonal carcinoma cell, hematopoietic stem cell, muscle stem cell, |
| XX | nerve stem cell, skin dermal sheath stem cell, liver stem cell or |
| XX | teratocarcinoma cell. The method involves contacting the stem cell with a |
| XX | stem-loop RNA molecule or a nucleic acid molecule or vector encoding the |
| XX | stem-loop RNA, where the nucleic acid is preferably derived from one of |
| XX | the nucleic acid sequences in AB261794-844, including the present |
| XX | sequence, and may encode a cell surface receptor expressed by a stem |
| XX | cell, or a ligand. The RNA molecule, the nucleic acid molecule or the |
| XX | vector is useful for promoting the differentiation of stem cells and for |
| XX | providing differentiated cells/tissues for the treatment of diseases in |
| XX | which cell/tissues are destroyed by the disease. These diseases include |
| XX | pernicious anaemia, stroke, neurodegenerative diseases such as |
| XX | Parkinson's disease and Alzheimer's disease, coronary heart disease, |
| XX | cirrhosis, diabetes, or nerve damage as a consequence of trauma (e.g. |
| XX | replacement of spinal cord tissue) (claimed) |
| XX | Sequence 1726 BP; 274 A; 631 C; 570 G; 231 T; 0 U; 0 Other; 0 |
| XX | SO |

```

Query Match      99.6%; Score 1577.2; DB 7; Length 1726;
Best Local Similarity 99.8%; Pred. No. 3.9e-276;
Matches 1579; Conservative 0; Mismatches 3; Indels 0; Gaps 0

```

[illegible]

5 TILSFA

RESULTS
ABZ81813

YD 3378
C107070

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ABZB
VV

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DT 11-3
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DE Liga

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|----------|---|---|------|
| Db | 1205 | GGGCAACCCAGAGAGAGGGTGCAGTCTCAGAGAGACTGCTGTGGCGTTCCACTGGTGC | 1264 |
| QY | 1141 | TGCGTAGTACAGTGCACACCGTCTCCGTTGTGCGCAAGAGACTCAGGCTCTGCGCTGTGACGC | 1200 |
| Db | 1265 | TGGGTAGTACAGTGCACACCGTTCGGGTGTGGCGCAGAGAGCTCAGGCTCTGCGCTGTGACGC | 1324 |
| QY | 1201 | GCGGCCCGGCGGTAGACTGACTTCGCGCAGCGGTGGCTCGCACTGTGGAGACTCAGGG | 1260 |
| Db | 1325 | GCGGCCCGGCGGTAGACTGACTTCGCGCAGCGGTGGCTCGCACTGTGGAGACTCAGGG | 1384 |
| QY | 1261 | CACGGCACCGGCGGCTCTGCGCGCTCGAGGCCAGGCTCTCCCTGCCAAGGCCCACTC | 1320 |
| Db | 1385 | CACGGCACCGGCGGCGCTCTGCGCGCTCGAGGCCAGGCTCTCCCTGCCAAGGCCCACTC | 1444 |
| QY | 1321 | CCAGGGCTCTGGAAATGGTGAAGCGCAGGGGCTTGAGAGAAACGCCCAACCAACGAGGCC | 1380 |
| Db | 1445 | CCAGGGCTCTGGAAATGGTGAAGCGCAGGGGCTTGAGAGAAACGCCCAACCAACGAGGCC | 1504 |
| QY | 1381 | AGGGGCCACAGACGGCCCGCAAAAAGCGCTCGGGAGCGTTTAAAGACATGTACAGGCC | 1440 |
| Db | 1505 | AGGGGCCACAGACGGCCCGCAAAAAGCGCTCGGGAGCGTTTAAAGACATGTACAGGCC | 1564 |
| QY | 1441 | CTCCCTCCCTTGGCTCTAGGAGGAACACAGTTTTTTTAGACTGGAATAAGCCAGTCTAA | 1500 |
| Db | 1565 | CTCCCTCCCTTGGCTCTAGGAGGAACACAGTTTTTTTAGACTGGAATAAGCCAGTCTAA | 1624 |
| QY | 1501 | AGGCTCTGGATACTGGGCTCCCCAGAACTGCTGGCCACAGATGGTGGTGAAGTTAGT | 1560 |
| Db | 1625 | AGGCTCTGGATACTGGGCTCCCCAGAACTGCTGGCCACAGATGGTGGTGAAGTTAGT | 1684 |
| QY | 1561 | ATCAATAAAGATATTTAAACA | 1582 |
| Db | 1685 | ATCAATAAAGATATTTAAACA | 1706 |
| RESULT 6 | | | |
| AAZ91783 | | | |
| ID | AAZ91783 standard; DNA; 1702 BP. | | |
| AC | AAZ91783; | | |
| XX | 01-JUN-2000 (first entry) | | |
| DT | Human Wnt-6 protein coding sequence. | | |
| DE | Human; Wnt-6 protein; Wnt-6-related disease; schizophrenia; epilepsy; | | |
| KW | bipolar disorder; unipolar disorder; Alzheimer's disease; cancer; | | |
| KW | squamous cell carcinoma; cardiovascular disease; stroke; diagnosis; | | |
| KW | developmental disorder; lamellar ichthyosis; therapy; ss. | | |
| OS | Homo sapiens. | | |
| PN | EP979870-Al. | | |
| PD | 16-FEB-2000. | | |
| PF | 27-OCT-1998; 98EP-00203616. | | |
| PR | 12-AUG-1998; 98GB-00017586. | | |
| PA | (SMK) SMITHKLINE BEECHAM PLC. | | |
| XX | | | |

Qy 1501 AGGCCTCTGGATACTGGGCTCCCAAGACTGCTGGCCACAGATGGTGGGTGAAGTTAGT 1560
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1625 AGGCCTCTGGATACTGGGCTCCCAAGACTGCTGGCCACAGATGGTGGGTGAAGTTAGT 1684
Qy 1561 ATCAATAAAGATATTAA 1578
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1685 ATCAATAAAGATATTAA 1702
Search completed: April 3, 2004, 03:02:01
Job time : 404.83 secs

GenCore version: 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.
QM nucleic - nucleic search, using sw model
Run on: April 3, 2004, 11:14:53 ; Search time 380.642 Seconds
(without alignments)
15564.412 Million cell updates/sec
Title: US-10-030-269A-5
Perfect score: 1584
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2466186 seqs, 1870095128 residues

Total number of hits satisfying chosen parameters: 4932372

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 1434.4 | 90.6 | 1754 | 10 | US-09-992-600A-83 |
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| | | | | | Sequence 18, Appl |
| | | | | | Sequence 83, Appl |
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| | | | | | Sequence 85, Appl |

ATTACHMENTS

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Qy 781 TCGGAGATCATGCCGGCTGGCGACCTGCTGGGAGAGCTGCCTCCATTTCCGAGGTTGGGC 840
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Search completed: April 4, 2004, 00:36:36

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.
QM nucleic - nucleic search, using sw model

Run on: April 3, 2004, 01:46:51 ; Search time 2679.85 Seconds
(without alignments)
17650.860 Million cell updates/sec

Title: US-10-030-269A-5
Perfect score: 1584
Sequence: 1 gcgtcgcgcgcgcgcact.....ataagatatttaaacacc 1584

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| c 23 | 470.8 | 29.7 | 475 | 9 | AI400680 | AI400680 tg98h04.x |
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| c 34 | 430 | 27.1 | 430 | 9 | AI378801 | AI378801 tc67c08.x |
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Job time : 2685.05 secs

OM nucleic - nucleic search, using sw model

Run on: April 3, 2004, 00:09:01 ; Search time 4071.25 Seconds
(without alignments)
16863.461 Million cell updates/sec

Title: US-10-030-269A-5
Perfect score: 1584
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940344

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| VERSION | AXI36323.1 GI:14272729 |
| DNA | 1584 bp |
| linear | PAT 30-MAY-2001 |

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
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Ota T., Isozaki T., Nishikawa T., Kawai Y., Sugiyama T. and
AUTHORS

TITLE Secretory protein or membrane protein
JOURNAL Patent: EP 1067182-A 245 10-JAN-2001;
Helix Research Institute (JP)

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| Qy | |
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| D6 | |

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LOCUS Homo sapiens cDNA PSEC0220 fls, clone HEMBA1005301, moderately
DEFINITION similar to Mouse Wnt-6 mRNA.
ACCESSION AK075522
VERSION AK075522.1 GI:22761718
KEYWORDS oligo capping; fls (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Ota, T., Nishikawa, T., Suzuki, Y., Kawai-Hiro, Y., Hayashi, K.,
Ishii, S., Saito, K., Yamamoto, J., Wakamatsu, A., Nagai, T.,
Nakamura, Y., Nagahara, K., Sugano, S. and Isogai, I.
HRI human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1584)
AUTHORS Isogai, T. and Yamamoto, J.
TITLE Direct Submission
JOURNAL Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yara, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass
sequencing, clone selection and full insert sequencing; Helix
Research Institute (supported by Japan Key Technology Center etc.);
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of Tokyo, Laboratory of Genome Structure, Human Genome Center.
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ORIGIN

Query Match 100.0%; Score 1584; DB 9; Length 1584;

Best Local Similarity 100.0%; Pred. No. 1.1e-213;

Matches 1584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5

AX565675

LOCUS

DEFINITION

ACCESSION

AX565675

Sequence 36 from Patent WO02077204.

AX565675

1726 bp

DNA

linear

PAT 29-NOV-2002

VERSION AX565675.1 GI:26000994

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 Andrews, P., Walsh, J. and Gokhale, P.

Stem cell

TITLE Patent: WO 02077204-A 36 03-OCT-2002;

JOURNAL

Axordia Limited (GB)

FEATURES

source

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Location/Qualifiers
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ORIGIN

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Best local Similarity 99.8%; Pred. No. 1e-212;
Matches 1579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 LOCUS AX597075
 DEFINITION Sequence 36 from Patent WO02090992.
 ACCESSION AX597075
 VERSION AX597075.1 GI:28397653
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 REFERENCE
 AUTHORS Andrews, P., Draper, J. and Walsh, J.
 TITLE Screening method
 JOURNAL Patent: WO 02090992-A 36 14-NOV-2002;
 Axordia Limited (GB)
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ORIGIN

Query Match 99.6%; Score 1577.2; DB 6; Length 1726;
 Best Local Similarity 99.8%; Pred. No. 1e-212;
 Matches 1579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGCTCGGGGGTTCGACTGAGCCCGGGGCGCTCGGGGCGCGGGTTCGCTCCCGCAGCC 60
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LOCUS AX701352 1726 bp DNA linear PAT 03-APR-2003
DEFINITION Sequence 2: from Patent WO03012082.
ACCESSION AX701352
VERSION AX701352.1 GI:29537001
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
AUTHORS Andrews, P., Walsh, J., and Gokhale, P.
TITLE Method for modulating stem cell differentiation using stem loop rna
JOURNAL Patent: WO 03012082-A 21 13-FEB-2003;
Axordia Limited (GB)

FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 99.6%; Score 1577.2; DB 6; Length 1726;
Best Local Similarity 99.8%; Pred. No. 1e-212;
Matches 1579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCCTCGCGCGCTCGACTGAGCGCGGGCCCTCGCGCGCGGTTGCGCCGAGCC 60
Db 125 CGCTCGCGCGCTCGACTGAGCGCGGGCCCTCGCGCGCGGTTGCGCCGAGCC 184
Qy 61 TCGCCCTCGCCACCGCGCGCGCGCTAGGCGGTACAGATGCTGCCGCGCTTACCTCC 120
Db 185 TCGCCCTCGCCACCGCGCGCGCGCTAGGCGGTACAGATGCTGCCGCGCTTACCTCC 244
Qy 121 CGCTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 245 CGCTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 304
Qy 181 GCTGTGGCAGCGCTTGTATGAGCCCTACAGCATCTGCAAGGAGGACGCGCGCTG 240
Db 305 GCTGTGGCAGCGCTTGTATGAGCCCTACAGCATCTGCAAGGAGGACGCGCGCTG 364
Qy 241 CGCGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 365 CGCGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 424
Qy 301 GCGCGCGCGCTCGGGGTGCGAGAGTGCCAGTTCCAGTTCCGCTGCGAATTGC 360

Db 425 GCGCGCGCGCTCGGGGTGCGAGAGTGCCAGTTCCAGTTCCGCTCGCGCGCTGGAATTGC 484
Qy 361 TCCAGCACAGCAAGCGCTTTGGAGCATCTTGCATACAGGACATTCGGGAGAGCGCTTTC 420
Db 485 TCCAGCACAGCAAGCGCTTTGGAGCATCTTGCATACAGGACATTCGGGAGAGCGCTTTC 544
Qy 421 GTGTTGGGCACTCTGCGGCGCGCGCGCAAGCGCTGCGAGAGGCTTCTATGCGGC 480
Db 545 GTGTTGGGCACTCTGCGGCGCGCGCGCAAGCGCTGCGAGAGGCTTCTATGCGGC 604
Qy 481 GAGCTGCTGCAATGCGGCTGCCAGCGCGCGCTGGCGGCGCTTCCCGCGCTTCCGCG 540
Db 605 GAGCTGCTGCAATGCGGCTGCCAGCGCGCGCTGGCGGCGCTTCCCGCGCTTCCGCG 664
Qy 541 CTGCGCGCGCAAGCGCGCGCGCTGGCGGCGCTTCCCGCGCTTCCCGCGCTTCCGCG 600
Db 665 CTGCGCGCGCAAGCGCGCGCGCTGGCGGCGCTTCCCGCGCTTCCCGCGCTTCCGCG 724
Qy 601 GAGTGGGAGGCTTGGCGGCGCGAGCTGAGCTTGGGAGAGGAGTCTTATG 560
Db 725 GAGTGGGAGGCTTGGCGGCGCGAGCTGAGCTTGGGAGAGGAGTCTTATG 784
Qy 661 GAGCGCGCGCAAGCGCGGCGCGAGCAATCGCGCGCTTGGTCAACTGCAACAAC 720
Db 785 GAGCGCGCGCAAGCGGCGCGAGCGCGAGCATCGCGGCTTGGTCAACTGCAACAAC 844
Qy 721 GAGCGCGCGCAAGCGCGGCTTGGCGGCGCGAGCAATCGCGCGCTTGGTCAACTGCAACAAC 780
Db 845 GAGCGCGCGCAAGCGCGGCTTGGCGGCGCGAGCGCGAGCTTGGTCAACTGCAACAAC 904
Qy 781 TCGGGATCATGCGGCTTGGCGGCGCGAGCAATCGCGGCTTGGTCAACTGCAACAAC 840
Db 905 TCGGGATCATGCGGCTTGGCGGCGCGAGCGCGAGCTTGGTCAACTGCAACAAC 964
Qy 841 GCGCGGCTGCTGAGAGGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCT 900
Db 965 GCGCGGCTGCTGAGAGGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCT 1024
Qy 901 GCGCTGCTGCGCGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCT 960
Db 1025 GCGCTGCTGCGCGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCT 1084
Qy 961 GCGGATTCGCGCGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCT 1020
Db 1085 GCGGATTCGCGCGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCT 1144
Qy 1021 GCGGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCT 1080
Db 1145 GCGGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCT 1204
Qy 1081 GCGGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCT 1140
Db 1205 GCGGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCT 1264
Qy 1141 TCGTGTAGTACATGCGCGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCT 1200
Db 1265 TCGTGTAGTACATGCGCGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCT 1324
Qy 1201 GCGGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCT 1260
Db 1325 GCGGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCTTCCAGCGCGCT 1384

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|----|------|--|------|
| Qy | 1261 | CACCGGACACGGGGGCTCTGGCCGCTCGAGCCACAGCCTCTCCCTGCCAAGCCCAATC | 1320 |
| Db | 1385 | CAOOGCACACGGGGGCTCTGGCCGCTCGAGCCCAAGCCTCTCCCTGCCAAGCCCAATC | 1444 |
| Qy | 1321 | CAAGGCTCTGGAATTGTGTGAGCGCAGGGGCTTGAGAGAAAGCCACACCAAGAGGCCT | 1380 |
| Db | 1445 | CCAGGGCTCTGGAATTGTGTGAGCGGAGGGGCTTGAGAGAAAGCCACACCAAGAGGCCT | 1504 |
| Qy | 1381 | AGGGGCGCAGACGGGCCCGAAGAAAGGGGCTCGGGGAGCGTTTAAAGACACTGTACAGGC | 1440 |
| Db | 1505 | AGGGGCGCAGACGGGCCCGAAGAAAGGGGCTCGGGGAGCGTTTAAAGACACTGTACAGGC | 1564 |
| Qy | 1441 | CTCCCTCCOCTTGGCCTCTAGAGGAAACAGTTTTATGACTGAAAAAAGCCACTTAA | 1500 |
| Db | 1565 | CTCCCTCCOCTTGGCCTCTAGAGGAAACAGTTTTATGACTGAAAAAAGCCACTTAA | 1624 |
| Qy | 1501 | AGGCTCTGGATACTGGGCTCCCGACACTGCTGCGACAGAGTGGTGGGTGAGGTTAGT | 1560 |
| Db | 1625 | AGGCTCTGGATACTGGGCTCCCGACACTGCTGCGACAGAGTGGTGGGTGAGGTTAGT | 1684 |
| Qy | 1561 | ATCAATAAGATATTAA | 1578 |
| Db | 1685 | ATCAATAAGATATTAA | 1702 |

Search completed: April 3, 2004, 11:14:11
Job time : 4080.45 secs

OM nucleic - nucleic search, using sw model

Run on: April 2, 2004, 21:47:00 ; Search time 396.83 Seconds
(without alignments)
16957.243 Million cell updates/sec

Title: US-10-030-269A-5
Perfect score: 1584
Sequence: 1 gcgcgcgcgcgcgcgcact.....ataagattattaaaccacc 1584

Scoring table: IDENTITY_NUC
Gapop 10.0 ; Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------|
| 1 | 1584 | 100.0 | 1584 | 4 | AAF29359 Amyloid-b |
| 2 | 1584 | 100.0 | 1584 | 5 | AAF93866 Human cDN |
| 3 | 1577.2 | 99.6 | 1726 | 7 | ABX75316 Human cDN |
| 4 | 1577.2 | 99.6 | 1726 | 7 | AAD52541 WNT-6 DNA |
| 5 | 1577.2 | 99.6 | 1726 | 7 | ABZ81813 Ligand WN |
| 6 | 1573.2 | 99.3 | 1702 | 3 | AAZ91783 Human wnt |
| 7 | 1434.4 | 90.6 | 1754 | 7 | ACC51101 Human Sol |
| 8 | 1434.4 | 90.6 | 1754 | 7 | ACC51102 Human Sol |
| 9 | 1333.8 | 84.2 | 1855 | 7 | ACC51108 Human Sol |
| 10 | 848.2 | 53.5 | 959 | 9 | ADD78265 Human CGD |
| 11 | 520 | 32.8 | 526 | 5 | AAF94068 Primer sp |
| 12 | 512 | 32.3 | 512 | 6 | ABS70488 Human bon |
| 13 | 466.6 | 29.5 | 803 | 4 | AAD16763 Human nov |

| | | | | | |
|----|-------|------|------|---|---------------------|
| 14 | 456.6 | 29.5 | 803 | 9 | ADC22055 Human cDN |
| 15 | 322 | 20.3 | 342 | 7 | AEZ36692 Human GEN |
| 16 | 213.2 | 13.5 | 1202 | 4 | AAD16767 Human nov |
| 17 | 213.2 | 13.5 | 1202 | 9 | ADC22059 Human cDN |
| 18 | 213.2 | 13.5 | 1228 | 3 | AAZ90451 Wnt-4AF a |
| 19 | 213.2 | 13.5 | 1515 | 7 | ABX62938 Human act |
| 20 | 213.2 | 13.5 | 1598 | 4 | AAI58045 Human pol |
| 21 | 211.6 | 13.4 | 1598 | 4 | AAI59831 Human pol |
| 22 | 211.6 | 13.4 | 2049 | 2 | AAZ34081 Human PRO |
| 23 | 211.6 | 13.4 | 2049 | 3 | AAZ78505 Human PRO |
| 24 | 211.6 | 13.4 | 2049 | 4 | AAZ45964 Human DNA |
| 25 | 211.6 | 13.4 | 2049 | 7 | ABX78567 Human PRO |
| 26 | 211.6 | 13.4 | 2049 | 7 | ACA75539 Novel hum |
| 27 | 211.6 | 13.4 | 2049 | 7 | ACA71019 Human sec |
| 28 | 211.6 | 13.4 | 2049 | 7 | ACC87547 Human sec |
| 29 | 211.6 | 13.4 | 2049 | 7 | ACC86933 Human sec |
| 30 | 211.6 | 13.4 | 2049 | 7 | ACD04106 Human sec |
| 31 | 211.6 | 13.4 | 2049 | 7 | ACA69437 cDNA enco |
| 32 | 211.6 | 13.4 | 2049 | 7 | ACA90282 Novel hum |
| 33 | 211.6 | 13.4 | 2049 | 7 | ACC9389 Human sec |
| 34 | 211.6 | 13.4 | 2049 | 7 | ACA98180 Novel hum |
| 35 | 211.6 | 13.4 | 2049 | 7 | ACA93822 Human sec |
| 36 | 211.6 | 13.4 | 2049 | 7 | ACD15215 Human: sec |
| 37 | 211.6 | 13.4 | 2049 | 7 | ACD08802 Human: sec |
| 38 | 211.6 | 13.4 | 2049 | 7 | ACC96722 Human sec |
| 39 | 211.6 | 13.4 | 2049 | 7 | ACF15443 Human sec |
| 40 | 211.6 | 13.4 | 2049 | 7 | ACD42614 Novel hum |
| 41 | 211.6 | 13.4 | 2049 | 7 | ACA72810 Human PRO |
| 42 | 211.6 | 13.4 | 2049 | 7 | ACD02982 Novel hum |
| 43 | 211.6 | 13.4 | 2049 | 7 | ACD01797 Novel hum |
| 44 | 211.6 | 13.4 | 2049 | 7 | ACA91989 Novel hum |
| 45 | 211.6 | 13.4 | 2049 | 7 | ACA63649 Novel hum |

ALIGNMENTS

RESULT 1

| | |
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| AAF29359 | AAF29359 standard; DNA; 1584 BP. |
| XX | |
| AC | AAF29359; |
| XX | |
| DT | 20-APR-2001 (first entry) |
| XX | |
| DE | Amyloid-beta protein agglutination regulating factor DNA SEQ ID 5. |
| XX | |
| KW | Human; amyloid-beta protein; agglutination regulatory factor: |
| KW | Alzheimer's disease; ds. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| PN | WO200104299-A1. |
| XX | |
| PD | 18-JAN-2001. |
| XX | |
| PF | 06-JUL-2000; 2000WO-JP004515. |
| XX | |
| PR | 08-JUL-1999; 99JP-00194179. |
| PR | 18-OCT-1999; 99US-0159586P. |
| XX | |
| PA | (HELI-) HELIX RES INST. |
| XX | |

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|---|--|
| PI | Ota T, Isogai T, Nishikawa T, Kawai Y, Yamazaki M, Satoh S; |
| PI | Arakawa H, Morita M; |
| XX | WPI; 2001-138347/14. |
| DR | P-PSDB; AAB49769. |
| DR | |
| XX | |
| PT | Polynucleotide encoding Amyloid-beta protein agglutination-controlling |
| PT | factor, useful for inhibiting or promoting agglutination or sedimentation |
| PT | of amyloid-beta protein and in diagnosis and screening drugs for |
| PT | Alzheimer's disease. |
| XX | |
| PS | Claim 1; Page 49-51; 72pp; Japanese. |
| XX | |
| CC | This invention relates to polynucleotides AAF29357 - AAF29361 which |
| CC | encode proteins AAB49767 - AAB49771. The proteins inhibit or promote the |
| CC | agglutination of amyloid beta protein. The protein and polynucleotide |
| CC | sequences are useful in the diagnosis of Alzheimer's disease. They are |
| CC | also useful for screening drugs which are useful for treating Alzheimer's |
| CC | disease |
| XX | |
| SQ | Sequence 1584 BP; 245 A; 572 C; 531 G; 236 T; 0 U; 0 Other; |
| Query Match 100.0%; Score 1584; DB 4; Length 1584; | |
| Best Local Similarity 100.0%; Pred. No. 2.3e-277; | |
| Matches 1584; Conservative 0; Mismatches C; Indels 0; Gaps 0; | |
| QY | 1 GGGCTCGGGCGCTCGACATGAAGACCCGGGGCCCTCGCGCGCGGGGTTGCGCCCGCAGCC 60 |
| DB | |
| DB | 1 GCGCTCGGGCGCTCGACATGAAGACCCGGGGCCCTCGCGCGCGGGTTGCGCCCGCAGCC 60 |
| QY | 61 TCGGCCCTTGCCACCCCGGGGGGGCGGTAGGGGGGTCAAGATGTGCGCGCCCTACCTCC 120 |
| DB | |
| DB | 61 TCGGCCCTTGCCACCCCGGGGGGGCGGTAGGGGGGTCAAGATGTGCGCGCCCTACCTCC 120 |
| QY | 121 CGCTCGGGCGTGTGCTGCTGCTGCTCTGTCGTGTCGCGGGCGACGTGCGGGGAGCTGTGGTGG 180 |
| DB | |
| DB | 121 CGCTCGGGCGTGTGCTGCTGCTGCTGCTGTCGTGTCGCGGGCGACGTGCGGGGAGCTGTGGTGG 180 |
| QY | 181 GCTGTGGGCGACGCCCTTGGTTATGACCCATACAGCATCTCGAGGAGGACGCGCGCGTG 240 |
| DB | |
| DB | 181 GCTGTGGGCGACGCCCTTGGTTATGACCCATACAGCATCTCGAGGAGGACGCGCGCGTG 240 |
| QY | 241 GCGGGCGGCGAGCGGAGTGTGTGCAGAGCTGAGCGGGAAGTGGTGGCAGAGCTAGCTCGG 300 |
| DB | |
| DB | 241 GCGGGCGGCGAGCGGAGTGTGTGCAGAGCTGAGCGGGAAGTGGTGGCAGAGCTAGCTCGG 300 |
| QY | 301 GCGCGCCCGGCTCGGGGTGCAGAGTGCACAGTCCAGCTTCAGTTCGCGCTTCGCGCGCTGGAATTC 360 |
| DB | |
| DB | 301 GCGCGCCCGGCTCGGGGTGCAGAGTGCAGAGTCCAGTTCAGTTCGCGCTTCGCGCGCTGGAATTC 360 |
| QY | 361 TCACGCCACAGCAAGGCCCTTTGAGGCATCCTGCACACAGGACATTCGGGAGAGCGGCTTC 420 |
| DB | |
| DB | 361 TCACGCCACAGCAAGGCCCTTTGAGGCATCCTGCACACAGGACATTCGGGAGAGCGGCTTC 420 |
| QY | 421 GTGTTTGGCCATCACTTGCGGCGCGGGCGCAGCCAGCCGTCAGCAGAGGCGCTGTCTATGGGC 480 |
| DB | |
| DB | 421 GTGTTTGGCCATCACTTGCGGCGCGGGCGCAGCCAGCCGTCAGCAGAGGCGCTGTCTATGGGC 480 |
| QY | 481 GAGCTGCTGCAGTGGGGCTGCACAGGCGCGCGGCTGGCGGGCGCCCTCCCGGCCCTCGGC 540 |
| DB | |
| DB | 481 GAGCTGCTGCAGTGGGGCTGCACAGGCGCGCGGCTGGCGGGCGCCCTCCCGGCCCTCGGC 540 |
| QY | 541 CTGGCCGCGCACCCCGGACGCCCTCTGGCCCGCGGGGCTCCCGGAGGACGCGCGCGCTGG 600 |

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| Db | 541 | CTGGCCGCGCACCCCGCGACCCCTGGCCCGCGGGGCTCCCGGAGGCGAGCGCGCGCTGG | |
| QY | 601 | GAGTGGGAGAGCTCGCGGCGACGAGCTGAGCTCTCGGGGAGCGAGAGTCSAGGCTCTTATG | |
| Db | 601 | GAGTGGGAGAGCTCGCGCGACGAGCTGAGCTCTCGGGGAGCGAGAGTCSAGGCTCTTATG | |
| QY | 661 | GAGCGCGCGCACAGCGGGGAGCGGAGAGCATCCGCGCGTGGTGCACTGCACACAC | 720 |
| Db | 661 | GAGCGCGCGCACAGCGGGGAGCGGAGAGCATCCGCGCGTGGTGCACTGCACACAC | 720 |
| QY | 721 | GAGCGCGCGCACGCTGGCGCTGCGGAGCGACACGCGCACCGAGTGCMAATGCCAGGGGTG | 780 |
| Db | 721 | GAGCGCGCGCACGCTGGCGCTGCGGAGCGACACGCGCACCGAGTGCMAATGCCAGGGGTG | 780 |
| QY | 781 | TCGGGATCATCGGGCTGGGCACTCTGCTGGGCGAGAGCTGCTTCATTTGGGGAAGTGGGCG | 840 |
| Db | 781 | TCGGGATCATCGGGCTGGGCACTCTGCTGGGCGAGAGCTGCTTCATTTGGGGAAGTGGGCG | 840 |
| QY | 841 | CGCGGCTGCTGGAGCGCTTCCACGGCGCTCCACGGCGCTCAGCGGCTATGGGCGACCAAGCGGCAAG | 900 |
| Db | 841 | CGCGGCTGCTGGAGCGCTTCCACGGCGCTCCACGGCGCTCAGCGGCTATGGGCGACCAAGCGGCAAG | 900 |
| QY | 901 | GCGCTGCTGGCGCCCGCTCCGCAAGCGCGCGCGCGCGAGCGGACCTCTCTAAGGCC | 960 |
| Db | 901 | GCGCTGCTGGCGCCCGCTCCGCAAGCGCGCGCGCGAGCGGACCTCTCTAAGGCC | 960 |
| QY | 961 | GCGGATTGCGCCGACTTCTGGCGCGCCCAACCGGACGCAACCGGCTCCCGGGGACGCGCGGT | 1020 |
| Db | 961 | GCGGATTGCGCCGACTTCTGGCGCGCCCAACCGGACGCAACCGGCTCCCGGGGACGCGCGGT | 1020 |
| QY | 1021 | CGCGGCTGCATAGCAGCGCGCGGACCTCAGCGGCTGCGACCTGCTGTGCTGCGCGCGCG | 1080 |
| Db | 1021 | CGCGGCTGCATAGCAGCGCGCGGACCTCAGCGGCTGCGACCTGCTGTGCTGCGCGCGCG | 1080 |
| QY | 1081 | GGGCAACCGCGAGAGAGGTCGAGTTCGAGAGACTGCTGTGGCGCTTCCACTGTGTGC | 1140 |
| Db | 1081 | GGGCAACCGCGAGAGAGGTCGAGTTCGAGAGACTGCTGTGGCGCTTCCACTGTGTGC | 1140 |
| QY | 1141 | TGGTAGTACAGTGCACCGCTGGCTGTGGCGAGGAGCTCAGGCTGTGCGCTTCCACTGTGTGC | 1200 |
| Db | 1141 | TGGTAGTACAGTGCACCGCTGGCTGTGGCGAGGAGCTCAGGCTGTGCGCTTCCACTGTGTGC | 1200 |
| QY | 1201 | GCGCGCCCGGCGGCTAGCTGACTTCGCGCAGGGGTGGCTCGCACCTGTGGGACCTCAGGG | 1260 |
| Db | 1201 | GCGCGCCCGGCGGCTAGCTGACTTCGCGCAGGGGTGGCTCGCACCTGTGGGACCTCAGGG | 1260 |
| QY | 1261 | CACGGGACCGGGCGGCTCTGGCGCTCGAGGCCAGGCTCTCGCTGCCAAGGCCCACTC | 1320 |
| Db | 1261 | CACGGGACCGGGCGGCTCTGGCGCTCGAGGCCAGGCTCTCGCTGCCAAGGCCCACTC | 1320 |
| QY | 1321 | CCAAGGCTCTGGMAATGTTGAGCGAGGGGCTTGAGAGGAAAGGCCACCGACCGAGGGCC | 1380 |
| Db | 1321 | CCAAGGCTCTGGMAATGTTGAGCGAGGGGCTTGAGAGGAAAGGCCACCGACCGAGGGCC | 1380 |
| QY | 1381 | AGGGGCGCAGACGGGCGCGAAAGGCGCTCGGGGAGCGTTTAAAGGACACTGTACAGGCC | 1440 |
| Db | 1381 | AGGGGCGCAGACGGGCGCGAAAGGCGCTCGGGGAGCGTTTAAAGGACACTGTACAGGCC | 1440 |
| QY | 1441 | CTCGCTCCCTTGGCTCTAGAGGAAACAGTTTTTAGACTGGAAAAGGCCAGCTCTAA | 1500 |
| Db | 1441 | CTCGCTCCCTTGGCTCTAGAGGAAACAGTTTTTAGACTGGAAAAGGCCAGCTCTAA | 1500 |

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|----|------|--|------|
| Qy | 1501 | AGGCGCTCTGGATACTGGGCTCCGACGAACCTGCTGGCCACAGGATGCTGGGTGAGGTTAGT | 1560 |
| Db | 1501 | AGGCGCTCTGGATACTGGGCTCCGACGAACCTGCTGGCCACAGGATGCTGGGTGAGGTTAGT | 1560 |
| Qy | 1561 | ATCAATAAAGATATTTAAACCAAC | 1584 |
| Db | 1561 | ATCAATAAAGATATTTAAACCAAC | 1584 |

RESULT 2

RESOLUT 2
AAFP3866
ID AAFP3866 standard; cDNA; 1584 BP.

AC AAF93866;

DT 23-MAY-2001 (first entry)

Human cDNA encoding a membrane or secretory protein clone pSEC0220

Human; secretory protein; membrane protein; vaccine; gene therapy;

XX
XX
XX rheum.acroid arthritis; diabetes; ss.[illegible]

PN
yy
EP106/182-A2.

PD 10-JAN-2001.

PF 07-JUL-2000; 2000EP-00114090.

PR 08-JUL-1999; 99JP-C0194179.

02-MAY-2000; 2000JP-00183766.

PA (HELI-) HELIX RES INST

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DR P-PSDB; AAB88439.

PT Nucleic acids encod

[illegible]

STAT# 1, SEX ID NO 245, 000pp + sequence LISTING; ENGLISH:
XX
XX

this invention relates to nucleic acid sequences AAF93744 - AAF93817
 which encode human secretory or membrane proteins represented by AAB88317
 - AAB89419. Included in the invention are primers AAF93917 - AAF94295 and
 AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the
 invention. The invention also includes methods for the production of
 antibodies directed against the proteins, and cDNA sequences, which can
 be used in vaccines. The polynucleotide sequences can be used in gene
 therapy. The polynucleotide sequences and the proteins they encode may be
 used in the prevention, treatment and diagnosis of diseases associated
 with inappropriate secretory protein/membrane protein expression. The
 nucleic acids and complementary sequences may also be used as DNA probes
 in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
 and quantitate the presence of similar nucleic acid sequences in samples.
 They may also be used to study the expression and function of secretory
 proteins/membrane polypeptides and their role in metabolism. The
 polypeptides may be used as antigens in the production of antibodies
 against them and in assays to identify modulators (agonists/ant

antagonists) of expression and activity. The antibodies and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g., by enzyme linked immunosorbent assay (ELISA). Examples of diseases which may be treated include rheumatoid arthritis and diabetes

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Query Match      100.0%; Score 1584; DB 5; Length 1584;
Best Local Similarity 100.0%; Pred. No. 2.3e-277;
Matches 1584; Conservative 0; Mismatches 0; Indels 0;
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[illegible]

Db 721 GAGGCGGCGAGCTGGCGCTGGCGAGCCACACGCGGACCGAGTGCATATGCGAGCGGCTG 780
 Qy 781 TCGGGATCATGCGGCGCTGGCGAGCTGGCGAGGAGAGCTGCATTCGCGAGGCTGGCG 840
 Db 781 TCGGGATCATGCGGCGCTGGCGAGCTGGCGAGGAGAGCTGCATTCGCGAGGCTGGCG 840
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 Db 841 GCGGCGCTGCTGGAGCGCTTCCACGGGCGCTCACGCGCTCATGCGGACCGACGCGCAG 900
 Qy 901 GCGCTGCTGGCGCGCTGGCGAGCTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
 Db 901 GCGCTGCTGGCGCGCTGGCGAGCTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
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 Db 1021 GCGGCTGCATAGCAGCGCGCGCGCGCGCTCAAGCGCGCGCGCGCGCGCGCGCGCG 1080
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 Db 1261 CACCGGCGAGCGCGCTGCGCGCTGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCG 1320
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 Db 1321 CAGGCGCTGCGGATGCTGAGCGAGGCGCTTGGAGGAGCGCGCGCGCGCGCGCGCGCG 1380
 Qy 1381 AGGCGCGCGAGCG 1440
 Db 1381 AGGCGCGCGAGCG 1440
 Qy 1441 CCGCTGCGCTTGGCTCTGAGGAGGAGAGCTTTTGGAGCTGGAAGGAGGAGGAGGAG 1500
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 Qy 1501 AGGCGCTGCGGATGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1560
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 Qy 1561 ATCAATAAGATATTAAACAC 1584
 Db 1561 ATCAATAAGATATTAAACAC 1584

RESULT 3
 ABX75316
 ID ABX75316 standard; cDNA; 1726 BP.
 XX

ABX75316;

25-MAR-2003 (first entry)
 Human cDNA encoding WNT-6.

Gene; Notch; Wnt; embryonic stem cell; embryogenesis; ss;
 differentiation; ligand; Parkinson's disease; Huntington's disease;
 motor neuron disease; heart disease; diabetes; liver disease; human;
 cirrhosis; renal disease; AIDS; acquired immunodeficiency syndrome.

Homo sapiens.

W0200277204-A2.

23-OCT-2002.

25-MAR-2002; 2002WC-GB001195.

23-MAR-2001; 2001GB-00007296.

23-MAR-2001; 2001GB-00007299.

17-APR-2001; 2001GB-00009346.

(AXOR-) AXORDTA LTD.

Andrews P, Walsh J, Gokhale P;

WP1; 2003-092852/08.

P-PSDB; ABU55888.

Modulating the differentiation of embryonic stem cells by providing ligands which bind receptors in the Notch and Wnt pathways, useful for treating diseases such as Parkinson's, Huntington's, heart disease, diabetes and AIDS.

Claim 3; Fig 42; 121pp; English.

The invention relates to modulating the differentiation of an embryonic stem cell, comprising: (a) providing a culture of embryonic stem cells; (b) providing at least one ligand or its active binding fragment, capable of binding its cognate receptor polypeptide expressed by the embryonic stem cell; (c) forming a culture comprising embryonic stem cells and the ligand; and (d) growing the cell culture. Also included are: (i) Modulating the differentiation of embryonic stem cells, comprising: (a) providing a cell transfected with a nucleic acid molecule selected from: (i) any of 9 fully defined Wnt nucleic acid sequences; (ii) a nucleic acid molecule that hybridises to the nucleic acid in (i), and which encodes a ligand capable of modulating embryonic stem cell differentiation, or capable of binding a Wnt receptor; or (iii) nucleic acid molecules which are degenerate as a result of the genetic code to the sequences of (i) or (ii); (b) forming a culture comprising the cell identified in (a) with an embryonic stem cell; and (c) growing the culture for the maintenance and/or differentiation of the embryonic stem cell; (2) inhibiting the differentiation of embryonic stem cells, comprising: (a) providing at least one polypeptide or its active fragment, that are inhibitors of the Wnt signalling pathway; (b) forming a culture comprising the cell identified in (a) with an embryonic stem cell; and (c) growing the culture for the maintenance of embryonic stem cells in an undifferentiated state; or (3) Inhibiting the differentiation of embryonic stem cells, comprising: (a) providing a cell transfected with a nucleic acid molecule selected from: (i) a molecule encoding a Wnt inhibitory polypeptide; (ii) a molecule which hybridises to the molecule of (i) and encodes a polypeptide capable of inhibiting Wnt signalling;

QY 1561 ATCAATAAAGATATTAAACCA 1582
D6 1695 ATCAATAAAGATATTAAACCA 1706

RESULT 4
RAD52541
ID AAD52541 standard; DNA; 1726 BP.

XX AAD52541;
XX 02-MAY-2003 (first entry)
XX WNT-6 DNA.

XX Drug screening; toxicology assay; signalling pathway; gene; WNT-6; ds.
XX Unidentified.

XX Key Location/Qualifiers
XX CDS 224..1321
XX /tag= a
XX /product= "WNT-6 protein"
XX /note= "This CDS has translation exceptions which alter
XX the reading frame"

XX W020029C992-A2.

XX 14-NOV-2002.

XX 29-APR-2002; 2002WO-GB001946.

XX 04-MAY-2001; 2001GB-00011004.

XX (AXOR-) AXORDIA LTD.

XX Andrews P, Draper J, Walsh J;

XX WPI; 2003-120579/11.

XX P-PSDB; AAE34043.

XX Identifying biologically active agents comprises cloning transfected
PT cells into a cell array, exposing the array to an agent to be tested, and
PT detecting signals generated by a reporter molecule as a result of
PT exposure to the agent.

XX Claim 19; Fig 36; 90pp; English.

XX The present invention relates to a novel screening method which enables
CC the identification of biologically active agents which mediate their
CC effect through the activation of genes. The method involves providing a
CC population of cells stably transfected with a nucleic acid encoding a
CC reporter molecule, cloning the transfected cells into a cell array,
CC exposing the array to at least one agent to be tested and detecting a
CC signal generated by the reporter molecule as a result of exposure to the
CC agent. The method is useful in identifying biologically active agents and
CC the genes through which the agents act, in screening potential drugs for
CC their ability to activate certain drug targets in a high-throughput
CC assay, in identifying relationships between signalling pathways and
CC specific signals that could be useful in eventually directing the
CC differentiation of embryonic stem cells and in toxicology assays by
CC testing for unwanted activation or inhibition of specific signalling
CC pathways. The present sequence is WNT-6 DNA used to illustrate the method

CC of the invention

XX Sequence 1726 BP; 274 A; 631 C; 570 G; 251 T; 0 U; 0 Other;

Query Match: 99.6%; Score 1577.2; DB 7; Length 1726;
Best Local Similarity 99.8%; Pred. No. 3.9e-276;
Matches 1579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCCTGGCGCGCTCCACTGAAGCCCGGGCCCTCGCCGCGCGGCTTGGCCCGCGAGCC 60
D6 125 GCCTCGCGCGCTCCACTGAAGCCCGGGCCCTCGCGCGCGGCTTGGCCCGCGAGCC 184
QY 61 TCGCCCGCTGCCACCCGGCGCGCTAGGGGGGTCAAGATGCTGCGCCCTTACCTCC 120
D6 185 TCGCCCGCTGCCACCCGGCGCGCTAGGGGGGTCAAGATGCTGCGCCCTTACCTCC 244
QY 121 CGCCTCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
D6 245 CGCCTCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 304
QY 181 GCTGTGGGAGCGCCCTTGGTTATGACCCCTACAGCATCTGCAAGAGCAAGCGGCTG 240
D6 305 GCTGTGGGAGCGCCCTTGGTTATGACCCCTACAGCATCTGCAAGAGCAAGCGGCTG 364
QY 241 GCGGGGCGGACGCGCGAGTGTGCGCAGGCTGAGCGGGAAGTGGTGGCAGGCTAGCTCG 300
D6 365 GCGGGGCGGACGCGCGAGTGTGCGCAGGCTGAGCGGGAAGTGGTGGCAGGCTAGCTCG 424
QY 301 GCGCGCCGCTCGGGGTGCGAGAGTGCAGTTCAGATTCGCGCTCCGCGCTGGAATTC 360
D6 425 GCGCGCCGCTCGGGGTGCGAGAGTGCAGTTCAGATTCGCGCTCCGCGCTGGAATTC 484
QY 361 TCCAGCCACAGCAAGGCTTTGGACGCAATCTGCAAGCAATTCGGGAGAGCGGCTTC 420
D6 485 TCCAGCCACAGCAAGGCTTTGGACGCAATCTGCAAGCAATTCGGGAGAGCGGCTTC 544
QY 421 GTGTTCGCAATCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
D6 545 GTGTTCGCAATCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 604
QY 481 GACTGCTGCAATCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
D6 605 GACTGCTGCAATCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 664
QY 541 CTGCGCGCGCACCCCGCGAGACCCCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
D6 665 CTGCGCGCGCACCCCGCGAGACCCCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 724
QY 601 GACTGCGGAGGCTGCG 660
D6 725 GACTGCGGAGGCTGCG 784
QY 661 GACGCGCGGACCAAGCGGCGGACCGCGAGACATTCGCGCGCGTGGTGCACCAACAC 720
D6 785 GACGCGCGGACCAAGCGGCGGAGACATTCGCGCGCGTGGTGCACCACTGCACCAAC 844
QY 721 GAGCGGCGGACGAGTGGCGGTGCGGAGGCGCAGCGCGCGCGCGCGCGCGCGCGCG 780
D6 845 GAGCGGCGGAGGCTGGCGGTGCGGAGGCGCAGCGCGCGCGCGCGCGCGCGCGCG 904
QY 781 TCGGATCATCGCGGTGCGCACTGCTGGCAGAGCTGCTCCATTTGCGAGGTTGGGC 840
D6 905 TCGGATCATCGCGGTGCGCACTGCTGGCAGAGCTGCTCCATTTGCGAGGTTGGGC 964

| | |
|----|---|
| XX | Ligand; WNT-5A; stem cell; stem-loop RNA; antianaemic; cerebroprotective; |
| XX | neuroprotective; nontropic; antiparkinsonian; cardiant; hepatotropic; |
| KW | antidiabetic; vulnary; gene therapy; gene; ds. |
| KW | Unidentified. |
| OS | |
| OS | |
| PN | W02003012082-A2. |
| PD | 13-FEB-2003. |
| XX | |
| XX | 25-JUL-2002; 2002WO-GE003409. |
| PF | 26-JUL-2001; 2001GB-00018223. |
| XX | (AXOR-) AXORDIA LTD. |
| PR | Andrews P, Walsh J, Gokhale P; |
| PA | WPI; 2003-2798398/27. |
| PA | |
| Pt | |
| Pt | |
| XX | Modulating the differentiation state of a stem cell, useful for treating |
| DR | e.g. pernicious anemia, stroke, cirrhosis, diabetes or a |
| XX | neurodegenerative disease, comprises contacting a stem cell with a stem |
| PT | loop RNA. |
| PT | |
| XX | Claim 7; Fig 23; 85pp; English. |
| PS | |
| XX | |
| XX | The present sequence is the nucleic acid sequence of ligand WNT-5A. The |
| OC | invention relates to a method of modulating the differentiation state of |
| OC | a stem cell, such as an embryonic stem cell, embryonic germ cell, |
| OC | embryonal carcinoma cell, haematopoietic stem cell, muscle stem cell, |
| OC | nerve stem cell, skin dermal sheath stem cell, liver stem cell or |
| OC | teratocarcinoma cell. The method involves contacting the stem cell with a |
| OC | stem-loop RNA molecule or a nucleic acid molecule or vector encoding the |
| OC | stem-loop RNA, where the nucleic acid is preferably derived from one of |
| OC | the nucleic acid sequences in AB281794-844, including the present |
| OC | sequence, and may encode a cell surface receptor expressed by a stem |
| OC | cell, or a ligand. The RNA molecule, the nucleic acid molecule or the |
| OC | vector is useful for promoting the differentiation of stem cells and for |
| OC | providing differentiated cells/tissues for the treatment of diseases in |
| OC | which cell/tissues are destroyed by the disease. These diseases include |
| OC | pernicious anaemia, stroke, neurodegenerative diseases such as |
| OC | Parkinson's disease and Alzheimer's disease, coronary heart disease, |
| OC | cirrhosis, diabetes, or nerve damage as a consequence of trauma (e.g. |
| OC | replacement of spinal cord tissue) (claimed) |
| XX | |
| XX | Sequence 1726 B2: 274 A; 631 C; 570 G; 251 T; 0 U; 0 Other? |

0:00:00 Match 99.6%: Score 1577.2: DB 7: Length 1726:

[illegible]

RESULT 5

ABZ81813

ID ABZ8

XXXX

AC ABZE

XX

DT 11-5

XX

DE Ligand WNT-5A nucleic acid sequence.

PI Barnes MR, Testa TT;
 XX WPI; 2000-197087/18.
 DR P-PSDB; AN81693.
 XX
 FT Novel polypeptide with Wnt-6 homology and its corresponding
 PT polynucleotide, useful for treating neurological, cardiovascular and
 PT developmental disorders.
 XX
 PS Claim 7; Page 13-14; 20pp; English.
 XX
 CC This sequence encodes the human Wnt-6 protein of the invention. The
 CC polynucleotides, polypeptides, agonists and antagonists are useful for
 CC treating Wnt-6-related diseases, e.g. schizophrenia, bipolar and unipolar
 CC disorder, Alzheimer's disease, epilepsy, cancer (particularly squamous
 CC cell carcinoma), cardiovascular disease, stroke, and developmental
 CC disorders (including lamellar ichthyosis). They can also be used for
 CC diagnosing (susceptibility to) diseases related to the expression of wnt-
 CC 6 by determining the presence of a mutation in the sequence encoding wnt-
 CC 6
 XX
 XX Sequence 1702 BP; 252 A; 629 G; 570 G; 251 T; 0 U; 0 Other;
 Query Match 99.3%; Score 1573.2; DB 3; Length 1702;
 Best Local Similarity 99.8%; Pred. No. 2e-275;
 Matches 1573; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GGCCTCGCGCGCTCGCACTGAAGCCCGGCGCCCTCGCGCGCGCGGTTGCGCCCGCAGCC 60
 DB 125 GGCCTCGCGCGCTCGCACTGAAGCCCGGCGCCCTCGCGCGCGCGGTTGCGCCCGCAGCC 184
 QY 61 TCGCCCGCTCGCCACCCCGGCGCGCTAGGCGCGTCAAGATGCTGCGCGCTTACCTCC 120
 DB 185 TCGCCCGCTCGCCACCCCGGCGCGCTAGGCGCGTCAAGATGCTGCGCGCTTACCTCC 244
 QY 121 CGCCTCGGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
 DB 245 CGCCTCGGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 304
 QY 181 GCTGTGGCGACGCCCTTGGTATGAGACCTTACAGCATCTGCAAGAGGCAAGCGCGGCTG 240
 DB 305 GCTGTGGCGACGCCCTTGGTATGAGACCTTACAGCATCTGCAAGAGGCAAGCGCGGCTG 364
 QY 241 GCGCGCGCGCGCGCGCGCTGTGCGAGGCTGAGCGAGTGGTGGCAGAGCTAGCTGG 300
 DB 365 GCGCGCGCGCGCGCGCGCTGTGCGAGGCTGAGCGAGTGGTGGCAGAGCTAGCTGG 424
 QY 301 GCGCGCGCGCTCGGCTGCGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
 DB 425 GCGCGCGCGCTCGGCTGCGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 484
 QY 361 TCCAGCCACAGAGCGCTTGGAGCGCATCTGCAAGAGGCAATTCGGGAGAGCGGCTTC 420
 DB 485 TCCAGCCACAGAGCGCTTGGAGCGCATCTGCAAGAGGCAATTCGGGAGAGCGGCTTC 544
 QY 421 GTGTTGCGCATCACTGCG 480
 DB 545 GTGTTGCGCATCACTGCG 604
 QY 481 GAGCTGCTCAGTGCAGTGCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
 DB 605 GAGCTGCTCAGTGCAGTGCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 664

QY 541 CTGGCCGGGCAACCCCGCGGAGACCCCTGGCCCGCGGGCTCCCGGGAAGGCGCGCGCGCTGG 600
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 QY 601 GAGTGGGAGGCTCGGCGACGACCTGAGCTTGGGAGGAGAGAGTGGAGGCTCTTTATG 660
 DB 725 GAGTGGGAGGCTCGGCGACGACCTGAGCTTGGGAGGAGAGAGTGGAGGCTCTTTATG 784
 QY 661 GAGCGGCGCACAGCGGAGCGCGAGCAATCCGCGGCTTGGTGGCACTGCACACAGAC 720
 DB 785 GAGCGGCGCACAGCGGAGCGCGAGCAATCCGCGGCTTGGTGGCACTGCACACAGAC 844
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 DB 905 TCGGATCATGCGCGCTGCGACCTGCTGCGAGAGTGGCTCCATTTGCGAGGTTGGG 864
 QY 841 GCGCGGCTGCTGAGGGCTTCCAGCGGCGCTCAGCGCTGCTGGCGACGACGCGCGAG 900
 DB 965 GCGCGGCTGCTGAGGGCTTCCAGCGGCGCTCAGCGCTGCTGGCGACGACGCGCGAG 1024
 QY 901 GCGCTGCTCGCGCGCTCGCGACGCTCAGCGCGCGCGCGCGAGCGAGCTCTCTCTAGCGCC 960
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 DB 1085 GCGGATTCGCGCGCTTCTGGCGCCCGCAACCGCGACCGGCTCCCGCGGACGCGCGGT 1144
 QY 1021 GCGGCTGCTATAGCAGCGCGCGGACCTCAGCGCGCTGCGAGCTGCTGCTGCTGCGCGCGC 1080
 DB 1145 GCGGCTGCTATAGCAGCGCGCGGACCTCAGCGCGCTGCGAGCTGCTGCTGCTGCGCGCGC 1204
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 QY 1141 TCGGTAGTACAGTGCACCGGCTGCGGTGTGGGAGAGAGTCAAGCTGCTGCTGCTGAGCC 1200
 DB 1265 TCGGTAGTACAGTGCACCGGTTGCGGTGTGGGAGAGAGTCAAGCTGCTGCTGCTGAGCC 1324
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 QY 1261 CACGCGACCGGCGCGCTCTGCGCTGAGCGCGAGCTCTGCTGCGCGCGCGCGCGCGCTG 1320
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QY 1501 AGGCGCTCTGGATACTGGGCTGCCAGAACTGCTGGCCACAGGATGGTGGGTGAGGTTAGT 1560
Db |||||||ACTGCTGGGCTGCCAGAACTGCTGGCCACAGGATGGTGGGTGAGGTTAGT 1684
QY 1561 ATCAATAAAGATATTAA 1578
Db |||||||ACTGCTGGGCTGCCAGAACTGCTGGCCACAGGATGGTGGGTGAGGTTAGT 1684
1685 ATCAATAAAGATATTAA 1702

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Job time : 404.83 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 4932372

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query % | | | ID | Description |
|---------------|------------|-------|--------|----------------------|-------------------|
| | Score | Match | Length | | |
| 1 | 1577.2 | 99.6 | 1726 | 14 US-10-285-976-18 | Sequence 15, Appl |
| 2 | 1434.4 | 90.6 | 1754 | 10 US-09-992-600A-83 | Sequence 83, Appl |
| 3 | 1434.4 | 90.6 | 1754 | 10 US-09-992-600A-85 | Sequence 85, Appl |
| 4 | 1434.4 | 90.6 | 1754 | 10 US-09-924-340-83 | Sequence 83, Appl |
| 5 | 1434.4 | 90.6 | 1754 | 10 US-09-924-340-85 | Sequence 85, Appl |

D6 785 GACGCGGCGCACAAAGCGGGACGCGGAGACATCCGCGGCTTGGTGCACACTGCAACAACAC 844
QY 721 GAGCGGGGCAAGCTGCGCGTGGCGAGCCACACGCGCACCGAGTGCATAATGCCACGCGGCTG 780
D6 845 GAGCGGGGCGAGGCTGCGCGTGGCGAGCCACACGCGCACCGAGTGCATAATGCCACGCGGCTG 904
QY 781 TCGGATCATGCGCGCTCGCGACCTGCTGGCAGAACTGCGCTCCATTTGGCGAGTGGGC 840
D6 905 TCGGATCATGCGCGCTCGCGACCTGCTGGCAGAACTGCGCTCCATTTGGCGAGTGGGC 964
QY 841 GCGCGGCTGCTGGAGGCTTCCACAGCGGCGCTCAGCGGCTCATGGGCAACAGCGGCAAG 900
D6 965 GCGCGGCTGCTGGAGGCTTCCACAGCGGCGCTCAGCGGCTCATGGGCAACAGCGGCAAG -024
QY 901 GCGCTGCTGGCGCGCTGCGCACGCTCAAGCGCGCGCGCGAGCGGAGCGCTCTCTACGCG 960
D6 1025 GCGCTGCTGGCGCGCTGCGCACGCTCAAGCGCGCGCGAGCGGAGCGCTCTCTACGCG 1084
QY 961 GCGCATTTGCGCGGACTTCTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020
D6 1085 GCGCATTTGCGCGGACTTCTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1144
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2004, 00:09:01 ; Search time 7754.39 Seconds
(without alignments)
16863.481 Million cell updates/sec

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Perfect score: 3017
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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41: em_hgt_other:*

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| 1 | 3017 | 100.0 | 3017 | 6 | AX136405 Sequence |
| 2 | 3017 | 100.0 | 3017 | 6 | BD033297 Amyloid b |
| 3 | 3017 | 100.0 | 3017 | 6 | BD123655 Secretary |
| 4 | 3017 | 100.0 | 3017 | 9 | AK075542 Homo sapi |
| 5 | 2997 | 99.3 | 3045 | 6 | AX877451 Sequence |
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| 7 | 2997 | 99.3 | 3045 | 9 | AK027717 Homo sapi |
| 8 | 2987.6 | 99.0 | 3042 | 9 | AF236056 Homo sapi |
| 9 | 2979.6 | 98.8 | 3031 | 9 | BC001740 Homo sapi |
| 10 | 2878 | 95.4 | 2986 | 9 | AK075557 Homo sapi |
| 11 | 2876 | 95.3 | 3174 | 6 | AF243848 Sequence |
| 12 | 2876 | 95.3 | 3174 | 6 | BD223150 98 human |
| 13 | 2744.8 | 91.0 | 2962 | 6 | AX747818 Sequence |
| 14 | 2744.8 | 91.0 | 2962 | 9 | AK092943 Homo sapi |
| 15 | 2045 | 67.8 | 2143 | 6 | AX400638 Sequence |
| 16 | 2045 | 67.8 | 2143 | 6 | AX013142 Sequence |
| 17 | 2045 | 67.8 | 2143 | 6 | BD206323 Human nuc |
| 18 | 1730.6 | 57.4 | 160115 | 9 | AL161447 Human DNA |
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| 21 | 1507.4 | 50.0 | 2319 | 6 | AX018185 Sequence |
| 22 | 1507.4 | 50.0 | 2319 | 6 | BD134998 Human nuc |
| 23 | 1507.4 | 50.0 | 2319 | 6 | BD206397 Human nuc |
| 24 | 1427.4 | 47.3 | 1429 | 6 | AX464352 Sequence |
| 25 | 1427.4 | 47.3 | 1429 | 6 | AX697031 Sequence |
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| 34 | 629 | 20.8 | 3534 | 10 | BC011152 Mus muscu |
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| 38 | 501.8 | 16.6 | 553 | 6 | AX136734 Sequence |
| 39 | 501.8 | 16.6 | 553 | 6 | BD123974 Secretary |
| 40 | 460.2 | 15.3 | 472 | 6 | BD242249 Compounds |
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ALIGNMENTS

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AX136405
LOCUS 3017 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 327 from Patent EP1067182.
ACCESSION AX136405
VERSION AX136405.1 GI:14272809

KEYWORDS

source Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Ota,T., Isegai,T., Nishi,Kawa,T., Kawai,Y., Sugiyama,T. and

AUTHORS

Hayashi,K.

Secretory protein or membrane protein

Patent: EP 1067182-A 327 10--JAN-2001;

Helix Research Institute (JP)

FEATURES

Location/Qualifiers

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/notes="unnamed protein product"

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 3017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| LOCUS | | | | |
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[illegible]

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JP 2002017376-A/164.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3017)
Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
Secretory protein or membrane protein
Patent: JP 2002017376-A 164 22-JAN-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017376-A/164
PD 22-JUN-2002
PF 07-JUL-2000 JP 2000253173
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PJ SUGIYAMA,
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RESULT 4
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LOCUS AK075542 3017 bp mRNA linear PRI 03-SEP-2002
DEFINITION Homo sapiens cDNA PSEC0242 fls, clone NT2RP3000266.
ACCESSION AK075542
VERSION AK075542.1 GI:22761755
KEYWORDS oligo capping; fls (full insert sequence).
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Kawai-Hiro,Y., Hayashi,K.,
Ishii,S., Saito,K., Yamamoto,J., Wakamatsu,A., Nagai,T.,
Nakamura,Y., Nagahara,K., Sugano,S. and Isegai,T.
TITLE HRI human cDNA sequencing project
JOURNAL Unpublished
2 (bases 1 to 3017)
AUTHORS Isegai,T. and Yamamoto,J.
TITLE Direct Submission
JOURNAL Submitted (20-MAR-2002) Takao Isegai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass
sequencing, clone selection and full insert sequencing; Helix
Research Institute (supported by Japan Key Technology Center etc.);
cDNA library construction; Institute of Medical Science, University
of Tokyo, Laboratory of Genome Structure, Human Genome Center.
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Query Match 100.0%; Score 3017; DB 9; Length 3017;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 3001 AATGTTCTGTCAACTT 3017
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Ax877451 3045 bp DNA linear PAT 17-DEC-2003
LOCUS Sequence 12356 from Patent EP1074617.
DEFINITION Ax877451
ACCESSION Ax877451.1 GI:40032187
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Ota, T., Iwagai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
TITLE Primers for synthesizing full-length cDNA and their use
JOURNAL Patent: EP 1074617-A 12356 07-FEB-2001;
Research Association for Biotechnology (JP)
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DB 150 TTCTCAGCGCTGATTTTGAAGTATGGGCTTGGGAACGGGCGTCCGAGCATGAAGTCGG 209
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QY 241 TTGGAGCTCCCGGAGCGCTGGAGCTCCAGACAGCGATCATGAGCTGGAGCGAGGCTCC 300
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RESULT 6
BD156664

LOCUS BD156664 3045 bp DNA linear PAT 17-JAN-2003
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD156664
VERSION BD156664.1 GI:27862422
KEYWORDS JP 2002191363-A/11507.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1. (bases 1 to 3045)
Ota,T., Isozaki,Y., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002191363-A 11507 09-JUL-2002;
HELIIX RESEARCH INSTITUTE
COMMENT CS Homo sapiens (human)
PN JP 2002191363-A/11507
PD 09-JUL-2002
PF 28-JUL-2000 JP 200280990
PI TOSHIO OTA, TAKAO ISOZAKI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KELLCHI NAGAI, TETSUJI OTSUKI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10, C12P21/02, C12Q1/68, C12P21/09, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key

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source
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DB 750 AGGACCTGAGCGAGTGCATCAATCAGATGAAAGAGGTGAGGAAACAGTGTGAGAGGAG 809
QY 781 GCGTGCACACACAGAGGTGCACAAAGGGGAGGAGGAAACGTTGCTTGGTAAACGAAAGTCCC 840
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QY 841 AGACACAGCGCGCGAGTTCGAGAGTGGTTTGGATTCAAGAGAGCAAGTGTGAGAAAGAGG 900
DB 870 AGACACAGCGCGCGAGTTCGAGAGTGGTTTGGATTCAAGAGAGCAAGTGTGAGAAAGAGG 929
QY 901 AAGACCAATGAGATCCAGTGGTGAATCAGAGAGCTCAGAGGAGCAGGCTGCGCGAGGAGC 960
DB 930 AAGACCAATGAGATCCAGTGGTGAATCAGAGAGCTCAGAGGAGCAGGCTGCGCGAGGAGC 989
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| RESULT 7 | AK027717 | AK02777-7 | 3045 bp | mRNA | linear | PRI 01-AUG-2002 |
| LOCUS | | | | | | |
| DEFINITION | | Homo sapiens cDNA F.74811 fis, clone NT2RP4001975, highly similar to Homo sapiens golgi membrane protein GF73 mRNA. | | | | |
| ACCESSION | AK027717 | | | | | |

RESULT 7
AK027717
LOCUS
DEFINITION
ACCESSION

VERSION
 keywords
 SOURCE
 ORIGIN
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 FEATURES
 source
 ORIGIN

AK027171.1 GI:14042605
 oligo capping; fls (full insert sequence).
 Homo sapiens
 Homo sapiens (human)
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 Isegai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
 Nishikawa,T., Nagai,K., Sugeno,S., Ishibashi,T., Fujimori,K.,
 Tanai,H., Kinata,M., Watanabe,M., Hi-zaoka,S., Ishii,S., Kawai,Y.,
 Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahara,K.,
 Masuho,Y. and Kanehori,K.
 NEDO human cDNA sequencing project
 Unpublished
 2 (bases 1 to 3045)
 Isegai,T. and Otsuki,T.
 Direct Submission
 Submitted (10-MAY-2001) Takao Isegai, Helix Research Institute,
 Genomics Laboratory; 1332-3 Yana, Misarazu, Chiba 292-0812, Japan
 (E-mail:genomics@hri.co.jp, Tel:81-438-32-3975, Fax:81-438-52-3986)
 NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert construction,
 Research Association for Biotechnology; cDNA library construction,
 5'- & 3'-end one pass sequencing and clone selection: Helix
 Research Institute (supported by Japan Key Technology Center etc.)
 and Department of Virology, Institute of Medical Science,
 University of Tokyo.
 Location/Qualifiers
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 /note="cloning vector: pHE18SFL3-mRNA from NT2 neuronal
 precursor cells after 2-weeks retinoic acid (RA)
 induction."

ORIGIN
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 Best Local Similarity 99.8%; P:0.0;
 Matches 3011; Conservative 5; Mismatches 1; Gaps 1;

QY 1 GCTGGGCGCAGCGGCGGAGCCGCGGAGCTTCGAGCGCGGCGGAGCGAGCGACC 60
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 DB 90 CGGGCGGCGCTCGTAGCGGGGCGCCCGGATCCCGAGTGGCGGCGCGAGCTTCGGAAGAAGA 149
 QY 121 TTCTCAGCGCTGATTTGATGATGATGGGCTTGGGAACGGGGGTGCGACGATGAAGTCGC 180
 DB 150 TTCTCAGCGCTGATTTGATGATGATGGGCTTGGGAACGGGGGTGCGACGATGAAGTCGC 209
 QY 181 CGCCCTCGTCTGGCGCCGCTGGTGGGCTGCATCTGCTTTGGGCTTCAACTCTGGA 240
 DB 210 CGCCCTCGTCTGGCGCCGCTGGTGGGCTGCATCTGCTTTGGGCTTCAACTCTGGA 269
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1470 AATAAATGTPACATCTGAGATGATTAATGTGAATTTTASTATGCACTTTGTAGAA 1529
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| | | | | | |
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| LOCUS | AF236056 | 3042 bp | mRNA | linear | PFI 08-JUN-2000 |
| DEFINITION | Homo sapiens golgi membrane protein GP73 mRNA, complete cds. | | | | |
| ACCESSION | AF236056 | | | | |
| VERSION | AF236056.1 | GI:7271866 | | | |
| KEYWORDS | . | | | | |
| SOURCE | Homo sapiens (human) | | | | |
| ORGANISM | Homo sapiens | | | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | |
| REFERENCE | 1 (bases 1 to 3042) | | | | |
| AUTHORS | Kladney,R.D., Bulla,G.A., Guo,L., Mason,A.L., Tollefson,A.E., Simon,D.J., Koutoubi,Z. and Fimmel,C.J. | | | | |
| TITLE | GP73, a novel Golgi-localized protein upregulated by viral infection | | | | |
| JOURNAL | Gene 249 (1-2), 53-65 (2000) | | | | |
| MEDLINE | 20293047 | | | | |
| PubMed | 10831838 | | | | |
| REFERENCE | 2 (bases 1 to 3042) | | | | |
| AUTHORS | Fimmel,C.J. and Kladney,R.D. | | | | |
| TITLE | Direct Submission | | | | |
| JOURNAL | Submitted (16-FEB-2000) Internal Medicine, St Louis University, 3635 Vista Ave. at Grand Blvd., St. Louis, MO 63110-0250, USA | | | | |
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| ORIGIN | | | | | |
| Query Match | 99.0%; Score 2987.6; DB 9; Length 3042; | | | | |
| Best Local Similarity | 99.8%; Prid.No. 0; | | | | |
| Matches 3012; | Conservative 0; Mismatches 4; Indels 2; Gaps 2; | | | | |
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| Dd | | | | | |
| | 8 GTTGCGGCACAGCGCGGAGACCGCGCCCGAGACTCGAGGCGCGCGCGCGAGCGACC 67 | | | | |
| Qy | 61 CGGGCGCGCTCGTAGCGGGSCCGCGGATCCCGAGTTCGCCGAGTGGCGGGCCGAGA 120 | | | | |
| Dd | 68 CGGGCGGGCTCGTAGCGGGGCGCCCGGTATCCCGAGTGGCGGGSCCGAGCGCTCGAAAAAGAGA 127 | | | | |
| Qy | 121 TTCTCAGCGCTGATTTTGAGATCATGGGCTTGGGAACGAGGGCGTGCAGCGTGAAGTCGC 180 | | | | |

Db 2947 C*CAATAAGTCTCTATTCACTCACTGTTAAATTTAGCAGATAGATTGCTGAGAAATA 3006

QY 300C AAATGTTCTGTTCAACTT 3017

Db 3007 AAATGTTCTGTTCAACTT 3024

RESULT 9

BC001740

LOCUS

DEFINITION Homo sapiens golgi phosphoprotein 2, transcript variant 1, mRNA

ACCESSION BC001740

VERSION BC001740.1 GI:12804630

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 3031)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Sherman,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marasina,K., Farmer,A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Aronson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.C., Munz,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettner,M., Madan,A., Young,A.C., Shvachenko,Y., Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shvachenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dicksen,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,J.S., Krzyzanski,M.I., Skalska,U., Smalios,D.E., Schmechel,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12477932

REFERENCE 2 (bases 1 to 3031)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (16-JAN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: mgc@nci.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNI)

DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Hsiao, Martin Krzyzanski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven

Ness, Pawan Pandoh, Arora-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smalius, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miramada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNI at: <http://image.llnl.gov>

Series: IRAL Plate: 6 Row: m Column: 7

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7706084.

FEATURES

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1. .3031

Location/Qualifiers

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1. .3031

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125..1327

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ORIGIN

Query Match 98.8%; Score 2979.6; DB 9; Length 3031;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2593; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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Db 1 GCCGGCGGAGAGCTCGAGAGCGCGGGCGGGGAGAGAGACCCGGGGGCGCTCTAGCGGG 60

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Db 61 GCGCGGATCCCGAGTGGCGGCGCGAGAGCTCGAAAAAGAGATTCTCAGCGCTGATTTCGA 120

QY 140 GATGATGGGCTTGGGAAACGGGCGCTCGAGAGCATGAATCGCGGGCGCCCTCTGCTGGCGCG 199

Db 121 GATGATGGGCTTGGGAAACGGGCGCTCGAGAGCATGAATCGCGGGCGCCCTCTGCTGGCGCG 180

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QY 260 GCACTCCAGACAGCATCATGAGCTGGAAAGGAGGCTCCGAGAGGGGGCTCGAGAGAG 319

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QY 1100 AGACCAAGCTTGTCAATCCCGAGCGACAGAGGAGGAGCAGGAAGCTGCCGGGAGAGGAG 1159
Db 1081 AGACCAAGCTTGTCAATCCCGAGCGACAGAGGAGGAGCAGGAAGCTGCCGGGAGAGGAG 1140
QY 1160 AAACCAAGCAAACTGAGAGAGGAAGTGACTACAACATGGATGAAATGAAAGCAATC 1219
Db 1141 AAACCAAGCAAACTGAGAGAGAGATGACTACAACATGGATGAAATGAAAGCAATC 1200
QY 1220 TGAAGACAGCAAGCAAGCGCTGCCAGGGGAATGACAGAAACATAGATGTCTTTAATCT 1279

Db 1201 TGAAGACAGCAAGCAAGCGCTGGCAGGGAATGACAGAAACATAGATGTCTTTAATCT 1260
QY 1280 TGAAGATCAGAAAGAGAGACCACTAAATTTACTTGTATCAAGCTGAAGAGCGGAATCATAC 1339
Db 1261 TGAAGATCAGAAAGAGAGACCACTAAATTTACTTGTATCAAGCTGAAGAGCGGAATCATAC 1320
QY 1340 ACTCTGAATTTGAATCGAATCACTATTTCAACAGGGGCGGAAGAGATGACTTTAAAT 1399
Db 1321 ACTCTGAATTTGAATCGAATCACTATTTCAACAGGGGCGGAAGAGATGACTTAAT 1380
QY 1400 GTTTCATGAGGAGCTGAATACTGAAAGCTGTGAATGTACTAAATAAATGTAACATCTGAA 1459
Db 1381 GTTTCATGAGGAGCTGAATACTGAAAGCTGTGAATGTACTAAATAAATGTAACATCTGAA 1440
QY 1460 GATGATTTATTTGTAATTTTAGTATGCACTTTGTGTAGGAAAAAATGGAATGGCTTTTA 1519
Db 1441 GATGATTTATTTGTAATTTTAGTATGCACTTTGTGTAGGAAAAAATGGAATGGCTTTTA 1500
QY 1520 AACAGCTTTTGGGGGCTACTTTGGAAGTGTCTAATAAGSTGTCACAATTTTGGTAGTAS 1579
Db 1501 AACAGCTTTTGGGGGCTACTTTGGAAGTGTCTAATAAGSTGTCACAATTTTGGTAGTAS 1560
QY 1580 GTATTTCTGAGAGCTCAACACCAAACTGGAACATAGTTCTCTCAAGTGTGGCA 1639
Db 1561 GTATTTCTGAGAGCTCAACACCAAACTGGAACATAGTTCTCTCAAGTGTGGCA 1620
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Db 1681 AGTCCATCTGCTGTGAAGGAGAGACAGAGAACTCTGGSTTCGGTCTGCTGTCAAGTGC 1740
QY 1760 TGTACAAAGTGTGTGTGCGAGCTGTACCTGTTCTCTCACTGAAAGTCTGGCTAATGCTC 1819
Db 1741 TGTACAAAGTGTGTGTGCGAGCTGTACCTGTTCTCACTGAAAGTCTGGCTAATGCTC 1800
QY 1820 TTGTGTAGTCACTTCTGATTTCTGACCAATCAATCAATGCGCTTAGACACTGACTGTT 1879
Db 1801 TTGTGTAGTCACTTCTGATTTCTGACCAATCAATCAATGCGCTTAGACACTGACTGTT 1860
QY 1880 AACACAAAGCTCACTAGCAAGTAGCAACAGCTTTAAGTCTAATAACAAAGCTGTCTGT 1939
Db 1861 AACACAAAGCTCACTAGCAAGTAGCAACAGCTTTAAGTCTAATAACAAAGCTGTCTGT 1920
QY 1940 GTGAGAAATTTTAAAGGCTACTTGTATATTAACCTTGTCAATTTTATGTACAAAC 1999
Db 1921 GTGAGAAATTTTAAAGGCTACTTGTATATTAACCTTGTCAATTTTATGTACAAAC 1980
QY 2000 GCTATTAAGTGGCTTAGAATTTGAACATTTGTGGTCTTTATTTACTTTGCTGTGTG 2059
Db 1981 GCTATTAAGTGGCTTAGAATTTGAACATTTGTGGTCTTTATTTACTTTGCTGTGTG 2040
QY 2060 GGCACAGCAACATTTCCCTAAATATATATTACCAAGAAAGCAAGAGAGTAGGTT 2119
Db 2041 GGCACAGCAACATTTCCCTAAATATATATTACCAAGAAAGCAAGAGAGTAGGTT 2100
QY 2120 TTTGACAAACAAACAGGCGCAAGGGGCTGACCTGGAGCAGACATGGTGAAGGCA 2179
Db 2101 TTTGACAAACAAACAGGCGCAAGGGGCTGACCTGGAGCAGACATGGTGAAGGCA 2160

OM nucleic - nucleic search, using sw model

Run on: April 2, 2004, 21:47:00 ; Search time 755.831 Seconds

(without alignments)
16957.243 Million cell updates/sec

Title: US-10-030-269A-7

Perfect score: 3017

Sequence: 1 gctgggcgcacgcgcggag.....taaaatgtctgttcaactt 3017

Scoring table: IDENTITY_NJC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002s:*

7: geneseqn2003as:*

8: geneseqn2003bs:*

9: geneseqn2003cs:*

10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | % Query | | | DB ID | Description |
|------------|---------|-------|--------|-------|--------------------|
| | Score | Match | Length | | |
| 1 | 3017 | 100.0 | 3017 | 4 | AAF29360 Amyloid-b |
| 2 | 3017 | 100.0 | 3017 | 5 | AAF93907 Human cDN |
| 3 | 2998.6 | 99.4 | 3051 | 3 | AAC64559 Human pro |
| 4 | 2998.6 | 99.4 | 3210 | 5 | ABV25476 Human pro |
| 5 | 2997 | 99.3 | 3045 | 4 | AH14672 Human cDN |
| 6 | 2987.6 | 99.0 | 3042 | 7 | ACC50169 Breast ca |
| 7 | 2987.6 | 99.0 | 3042 | 9 | ADB75331 Prostate |
| 8 | 2987.6 | 99.0 | 3042 | 9 | ADD18542 Human pro |
| 9 | 2921.8 | 96.8 | 3154 | 6 | ASQ99606 Human cod |
| 10 | 2899.4 | 96.1 | 4042 | 7 | ASZ35869 Human sec |
| 11 | 2876 | 95.3 | 3174 | 3 | AAB26421 Human sec |
| 12 | 2744.8 | 91.0 | 2962 | 9 | ADB63189 Human cDN |
| 13 | 2045 | 67.8 | 2143 | 2 | AAZ42062 Human end |

Search completed: April 3, 2004, 11:14:23

Job time : 7766.59 secs

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Qy 601 AGCACTGAGCGAGTGCAATCAAACAGATGAAGAGAGAGTGTGAGGAGCGAA 660
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Qy 661 TAGAAGAGGTCAACAAAAGGGGAGTGAAGTGTAGCTTCCAGAGAGCTGAGTGAAGAA 720
Db 661 TAGAAGAGGTCAACAAAAGGGGAGTGAAGTGTAGCTTCCAGAGAGCTGAGTGAAGAA 720
Qy 721 AGACCAAGAGACAGAGCTCCAGAGCCCTCAGTGAAGCTCAGCCAGAGCTGAGGAGCAG 780
Db 721 AGACCAAGAGACAGAGCTCCAGAGCCCTCAGTGAAGCTCAGCCAGAGCTGAGGAGCAG 780
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Db 761 GCTGCCACACACAGAGTGCACAAAGGGAAGGAAAGCTGTGTTGAAGAGAGCTCC 840
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Db 841 AGACCAAGCCCAAGTCCAGAGTGTGTTGAAGTGAAGAGAGAGTGTGAGAGAGG 900
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Db 1081 AGATGAGAGGCGCTGAGAGAGAGAGTGTGTTGAAGTGAAGAGAGAGTGTGAGAGAGG 1140
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Db 1141 AAGCTGCCGAGAGAGAGAGTGTGTTGAAGTGAAGAGAGAGTGTGAGAGAGG 1200
Qy 1201 ATGAAATGAGAGAGAGTGTGTTGAAGTGAAGAGAGAGTGTGAGAGAGG 1260
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Db 1261 ACATAGATGTTTAAATGTTGAAGTGAAGAGAGAGTGTGAGAGAGG 1320
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Db 1321 GTGAAAGGAGAGTGTGTTGAAGTGAAGAGAGAGTGTGAGAGAGG 1380
Qy 1381 GAGAGATGTTTAAATGTTGAAGTGAAGAGAGAGTGTGAGAGAGG 1440
Db 1381 GAGAGATGTTTAAATGTTGAAGTGAAGAGAGAGTGTGAGAGAGG 1440
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Db 1441 AATAAATGATCTGAGAGTGTGTTGAAGTGAAGAGAGAGTGTGAGAGAGG 1500

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Db 2401 TGAATTTACTACTTAAATCTTAATCAAGTAAATGCAATGCAATGCAATGCAATGCAAT 2460

08-JUL-1999; 99JP-001947479.
11-JAN-2000; 2000JP-00118775.
32-MAY-2000; 2000JP-00183766.
(HELI-) HELIX RES INST.
Ota T, Isegai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
WPI; 2001-093989/11.
P-PSD; AAB88480.
Nucleic acids encoding secretory proteins/membrane proteins, useful in
gene therapy or as candidate target molecules in drug development.
Claim 1; SEQ ID NO 327; 609pp + Sequence Listing; English.
This invention relates to nucleic acid sequences AAF93744 - AAF93916
which encode human secretory or membrane proteins represented by AAB88317
- AAB88419. Included in the invention are primers AAF93917 - AAF94295 and
AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the
invention. The invention also includes methods for the production of
antibodies directed against the proteins, and cDNA sequences, which can
be used in vaccines. The polynucleotide sequences can be used in gene
therapy. The polynucleotide sequences and the proteins they encode may be
used in the prevention, treatment and diagnosis of diseases associated
with inappropriate secretory protein/membrane protein expression. The
nucleic acids and complementary sequences may also be used as DNA probes
in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
and quantitate the presence of similar nucleic acid sequences in samples.
They may also be used to study the expression and function of secretory
proteins/membrane polypeptides and their role in metabolism. The
polypeptides may be used as antigens in the production of antibodies
against them and in assays to identify modulators (agonists and
antagonists) of expression and activity. The antibodies and antagonists
may also be used as therapeutic agents to down regulate expression and
activity. The antibodies may also be used as diagnostic agents for
detecting the presence of the polypeptides in samples (e.g. by enzyme
linked immunosorbent assay (ELISA)). Examples of diseases which may be
treated include rheumatoid arthritis and diabetes

Query Match 100.0%; Score 3017; DB 5; Length 3017;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 3017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCTGGCGCACGGCGCGGAGGCGGGCGGGCGCGGGAGAGCGAC 60

1 GCTGGGCGCAGGGCGCGGA GCCGGCCGGA GTTCAGGCCCGCGCGCGGAGAGCGCAC

61 CGGGGGGCGTGGTAGGGGGGGCCCGGATCCCGAGTGGGGCCGGAGCCTCGAAAAAGAGA 120

61 C G G C G G C C T C G T A G C G S G G C C C C G G A T C C C C G A G T G G C G S C G G A G C C T C G A A A G A G A 120

121 TTCTCAGCGGTGATTTT GAGATGATGGCTTGGGAAACGGGCGTGCCAGCATGAAGTCGC 180

121 TTCTACGGCTGATTTTGAGATGATGGCTTGGGAAACGGGGCTCGCAGCATGAATCGC 180

181 CGCCCTCGTGCTGGCGCCCTGGTGGCTGCATCATCGTCTTGGGCTTCAACTACTGA 240

181 GCGCCCTCGTCTGGCGGCCCTGGTGGCTTGCATCATGCTCTTGGGCTTCAACTACTGA 240

241 TTGGAGCTCCGGAGGGTGGACCTCCAGACACGGATCATGGAGCTGGAGGAGGGTCC 300

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Db 301 GCAGGCGCGCTGCAGAGAGAGCGCGCTGAGCTGAGAGAGAACGAGTTCAGGCGAGAGC 360
Qy 361 TGGAGAGCGAGCGGGAGAGCGCTTGAAGAAATCGAGTTCAGGCGAGAGC 420
Db 361 TGGAGAGCGAGCGGGAGAGCGCTTGAAGAAATCGAGTTCAGGCGAGAGC 420
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Db 421 GGGTCAACAGAGCTTACCGAGCGAGAGAGCGGCTTTGGTGAATAACATCAACACAGGTC 480
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Db 661 TAGAGAGAGTCAACAAAGAGGAGATGAAGCTGTAGCTTCCAGAGAGCGCTGAGTGAAGACA 720
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Db 721 ACGAGAGAGAGAGAGTCCAGGCTTCAGTGAAGCGCTCAGGCCAGAGCGCTGAGAGAGAG 780
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Db 781 GCGTGCACACAGAGAGTGCACAGGAGAGGAGAGAGTGTGGTAAACAGCAAGTCCC 840
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Qy 1681 TACAGCGCACATAGAGAGTCCATCTGCTGAGAGAGAGACAGAGAGCTTGGGTC 1740
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Db 1741 CGTCTCTCTGTCACAGCTGTACCAAGTGTGGTGGCAGCGCTGTACCTGTTCTCAGT 1800
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Db 1801 AAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATCTGACATCAATCAATCAATG 1860
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Qy 2041 TTACTTTGCTTGTGTGGGCAAGCAACATCTTCCCTAAATATATATTAACCAAGAAA 2100
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Qy 2101 GCAAGAGAGAGATGTTTTTGAACAAACAAACAGGCGGAGCTGACCTGGAGC 2160
Db 2101 GCAAGAGAGAGATGTTTTTGAACAAACAAACAGGCGGAGCTGACCTGGAGC 2160

AAC64559 standard; cDNA; 3051 bp.

XX AAC64559;
XX AC AAC64559;
XX 14-FEB-2001 (first entry)
XX DT Human prostate specific gene 30P3C8 nucleotide sequence SEQ ID NO:1.

XX DE Human; prostate specific gene; 30P3C8; prostate cancer; diagnosis;
XX KW cytotstatic; gene therapy; vaccine; tumour; ss.

XX OS Homo sapiens.

XX XX WO200061610-A2.

XX XX 19-OCT-2000.

XX XX 12-APR-2000; 2000WO-US010218.

XX XX 12-APR-1999; 99US-0128660P.

XX XX (UROS-) UROGENESYS INC.

XX PI Afar DE, Hubert RS, Leong K, Raitano AB, Saffran DC;

XX XX WPT; 2000-619224/59.

XX XX P-PSDB; A0524352.

XX XX 30P3C8 polypeptide and polynucleotide used for diagnosing, treating and
XX PT monitoring development of prostate cancer.

XX PS Claim 1; Page 92-94; 99pp; English.

XX CC The present sequence encodes the human prostate specific protein 30P3C8,
XX CC which is over-expressed in prostate cancer cells. 30P3C8 has cytostatic
XX CC activity and can be used in vaccines and gene therapy. Methods for
XX CC detecting the levels of 30P3C8 protein or mRNA in prostate tissue, bone
XX CC tissue, lymphatic tissue, serum, blood or semen are used for diagnosing
XX CC the presence of cancer in an individual or dysregulated cell growth e.g.
XX CC hyperplasia. The cancers which are detected or diagnosed are of the
XX CC bladder, pancreas, colon, brain, bone, lung, kidney or prostate by using
XX CC test samples of serum, blood or urine or tissues of the bladder,
XX CC pancreas, colon, brain, bone, lung, kidney and prostate. 30P3C8
XX CC polynucleotide sequences can be used for treating cancers expressing
XX CC 30P3C8, particularly prostate cancers. Immunogenic portions of 30P3C8 are
XX CC used in vaccines to inhibit the development of cancer. Anti-30P3C8
XX CC monoclonal antibodies bind to 30P3C8 and disrupt interactions between
XX CC 30P3C8 and other proteins e.g. receptors for which 30P3C8 is a ligand.
XX CC 30P3C8 may be a growth factor or other molecule involved in tumour growth
XX CC and metastasis and so anti-30P3C8 antibodies may disrupt the homing or
XX CC invasion or other cancer promoting activities of 30P3C8. The assays are
XX CC used for detecting, staging and monitoring prostate cancer. The 30P3C8
XX CC protein or mRNA are used as additional specific markers for detecting
XX CC prostate cancer and provide a more specific assay than the serum prostate
XX CC specific antigen (PSA) assay

XX SQ Sequence 3051 BP; 909 A; 638 C; 808 G; 696 T; 0 U; 0 Other;

Query Match 99.4%; Score 2998.6; DB 3; Length 3051;

Best Local Similarity 99.8%; Pred. No. 0;

Marches 3012; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 2161 AGAGCATGCTGAGAGGCAAGGCATGAGAGGCAAGTCTTTTGTGTCAGAGATCTGTGCTT 2220
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QY 2161 AGAGCATGCTGAGAGGCAAGGCATGAGAGGCAAGTCTTTTGTGTCAGAGATCTGTGCTT 2220
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2221 ACTTTATCTGAGTAAAGAAACAAAGTTCATTTGATGTCGAAGATATATACAGTCT 2280
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2221 ACTTTATCTGAGTAAAGAAACAAAGTTCATTTGATGTCGAAGATATATACAGTCT 2280
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2281 TAGAAATAGGACTGTTTAGAAAACAGGAATACAAATGCTTTTATCATAGTGTACA 2340
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2281 TAGAAATAGGACTGTTTAGAAAACAGGAATACAAATGCTTTTATCATAGTGTACA 2340
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2341 CATTTAGCTTGTGTAAATGACTCACAATACTGAATTTAAATCAAGTAAATGTAATTT 2400
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2341 CATTTAGCTTGTGTAAATGACTCACAATACTGAATTTAAATCAAGTAAATGTAATTT 2400
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2401 TAGAAATAGGACTGTTTAGAAAACAGGAATACAAATGCTTTTATCATAGTGTACA 2460
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2401 TAGAAATAGGACTGTTTAGAAAACAGGAATACAAATGCTTTTATCATAGTGTACA 2460
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2461 GGTCTTCTAGTATTTATTTGTAATAGGCTCTTACCACCTTGCATTAATGCTGCAATC 2520
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2461 GGTCTTCTAGTATTTATTTGTAATAGGCTCTTACCACCTTGCATTAATGCTGCAATC 2520
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2521 ATTAAATGACTGACTTCCAGTAAGGCTCTTAAAGGGTAAGTAGAGGATCCACAGATT 2580
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2521 ATTAAATGACTGACTTCCAGTAAGGCTCTTAAAGGGTAAGTAGAGGATCCACAGATT 2580
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2581 TGAGATGCTTAGGCCCCAGAGATGTTTGAACCAACCTCTTATTTTCAAGGGGAAAT 2640
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2581 TGAGATGCTTAGGCCCCAGAGATGTTTGAACCAACCTCTTATTTTCAAGGGGAAAT 2640
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2641 GGGGCTAGAGTTAGAGGATCTAGCTGGTGGTGGGCAACCTGGCTCCTACACAGAC 2700
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2641 GGGGCTAGAGTTAGAGGATCTAGCTGGTGGTGGGCAACCTGGCTCCTACACAGAC 2700
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2701 TCCGAGTAGCTGGGACTACAGGCAACAGTCACTGAGGCGGCCCTGTTTGCATTTCC 2760
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2701 TCCGAGTAGCTGGGACTACAGGCAACAGTCACTGAGGCGGCCCTGTTTGCATTTCC 2760
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2761 GCTGCCACTCCAACTTAACATCTTCTATGATGATGCTTCTAGTCACTAAGGTTAAAC 2820
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2761 GCTGCCACTCCAACTTAACATCTTCTATGATGATGCTTCTAGTCACTAAGGTTAAAC 2820
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2821 TTTCCCAACCAAGGCAACTTATAGATAAAATCTTAGAGTACTTTTATCTCTTAAG 2880
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2821 TTTCCCAACCAAGGCAACTTATAGATAAAATCTTAGAGTACTTTTATCTCTTAAG 2880
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2881 TCCCTCTCCAGCTCCTTTGAGTCTCTCTTGGGTTGATAGGATTTTCTCTGCTTC 2940
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2881 TCCCTCTCCAGCTCCTTTGAGTCTCTCTTGGGTTGATAGGATTTTCTCTGCTTC 2940
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2941 TCAATAAGTCTCTATTCACTCATGTTTAAATTTAGGCATAGAAATGCTGAGAAATA 3000
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2941 TCAATAAGTCTCTATTCACTCATGTTTAAATTTAGGCATAGAAATGCTGAGAAATA 3000
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 3001 AATGTTCTGTCAACTT 3017
Db |||||||||||||||||||
QY 3001 AATGTTCTGTCAACTT 3017
Db |||||||||||||||||||

QY 1 GCTGGGSCACGGGCGCGAGGCCGCGCGAGGCTCGAGGCGGCGCGCGGAGAGGAGCGC 60
Db 20 GCTGGGCGGCGAGCGCGGCGGAGGCTCGAGGCGGCGCGGCGGCGGAGAGGAGCGC 79
QY 61 CGGCGGCGCTCTAGCGGCGCGCGGATCCCGGAGTGGCGGCGGAGGCTCGAGAGAGAG 120
Db 80 CGGCGGCGCTCTAGCGGCGCGCGGATCCCGGAGTGGCGGCGGAGGCTCGAGAGAGAG 139
QY 121 TCTCAGCGCTGATTTGAGATGATGGGCTTGGGAAACGGGCGTGGGAGGATGAAGTCGG 180
Db 140 TCTCAGCGCTGATTTGAGATGATGGGCTTGGGAAACGGGCGTGGGAGGATGAAGTCGG 199
QY 181 CGCCCTCGTGGTGGCGCGCTGGTGGCTGCAATCATGCTTTGGGCTTCACTACTGGA 240
Db 200 CGCCCTCGTGGTGGCGCGCTGGTGGCTGCAATCATGCTTTGGGCTTCACTACTGGA 259
QY 241 TTGGAGAGCTCCCGGAGCGCTGGAGCTCCAGACAGCGATCATGAGTGGAGGCGAGGCTCC 300
Db 260 TTGGAGAGCTCCCGGAGCGCTGGAGCTCCAGACAGCGATCATGAGTGGAGGCGAGGCTCC 319
QY 301 GCAAGCGCGCTGCAGAGAGAGGCGCGTGGAGCTGAAGAAGAAAGAGTTCGAGGAGAGC 360
Db 320 GCAAGCGCGCTGCAGAGAGAGGCGCGTGGAGCTGAAGAAGAAAGAGTTCGAGGAGAGC 379
QY 361 TGGAGAGCGAGCGGAGAGAGCTTGAGCAAAATCCAGTCCAGGCCACACCTTCCAGCTGGAGA 420
Db 380 TGGAGAGCGAGCGGAGAGAGCTTGAGCAAAATCCAGTCCAGGCCACACCTTCCAGCTGGAGA 439
QY 421 SCGTCAACAGCTGTACAGAGAGGAAAGCGGCTTTGGTGAATAACATCAACACAGGTG 480
Db 440 GCGTCACAGAGCTGTACAGAGAGGAAAGCGGCTTTGGTGAATAACATCAACACAGGTG 499
QY 481 AGAGGCTCATCCAGGTGCTGCAAGAGCGATTAAGAAGCCCTGCAAGAGATTAAGCGGAGGC 540
Db 500 AGAGGCTCATCCAGGTGCTGCAAGAGCGATTAAGAAGCCCTGCAAGAGATTAAGCGGAGGC 559
QY 541 TCGAGAGAGAGCTCGAGTTCAGAGAGAGCGAGACCTGAGAGGAGAGGAGTCTCCT 600
Db 560 TCGAGAGAGAGCTCGAGTTCAGAGAGAGCGAGACCTGAGAGGAGAGTCTCCT 619
QY 601 ACCAGCTGAGCGAGTGCATCAATCAGATGAAGAGGCTGAAGGAAACAGTGTGAGAGCGGAA 660
Db 620 ACCAGCTGAGCGAGTGCATCAATCAGATGAAGAGGCTGAAGGAAACAGTGTGAGAGCGGAA 679
QY 661 TAGAGAGGTCAACAAAAGGGAATGAAGCTGTAGCTTCCAGAGAGCTGAGTGAAGAACA 720
Db 680 TAGAGAGGTCAACAAAAGGGAATGAAGCTGTAGCTTCCAGAGAGCTGAGTGAAGAACA 739
QY 721 ACCAGCAGAGAGAGAGCTCCAGAGCGCTCAGTGAAGCTCAGCGCTCAGCGAGAGAGAGCAG 780
Db 740 ACCAGCAGAGAGAGAGCTCCAGAGCGCTCAGTGAAGCTCAGCGCTCAGCGAGAGAGAGCAG 799
QY 781 GCTTGGCCACACAGAGAGTCCACAGAGGAAAGGAAAGCTTGGTGAACAGAGAGAGTCC 840
Db 800 GCTTGGCCACACAGAGAGTCCACAGAGGAAAGGAAAGCTTGGTGAACAGAGAGAGTCC 859
QY 841 AGACACAGCGCCCGAGTTCCAGAGTGGTTTGGATTCAAGAGAGAGAGTGAAGAAGAGG 900
Db 860 AGACACAGCGCCCGAGTTCCAGAGTGGTTTGGATTCAAGAGAGAGAGTGAAGAAGAGG 919
QY 901 AAAACCAATGAGATCCAGGTGATGAGGAGCGCTCAGAGGAGAGGCTGCGCGAGAGC 960
Db 920 AAAACCAATGAGATCCAGGTGATGAGGAGCGCTCAGAGGAGAGGCTGCGCGAGAGC 979

QY 961 CAGGCGCGGAGAGAGGCTGTGGAGAGAGAGAGCTGTGGAGAGAGGCTTGGGAGAGCGC 1020
Db 980 CAGGCGCGGAGAGAGGCTGTGGAGAGAGAGAGCTGTGGAGAGAGGCTTGGGAGAGCGC 1039
QY 1021 CAGAACTGGGCGCAGACCCCAAGGTCAGGCTGCCCTGTCACTGAGCCAGGAAATCCAG 1080
Db 1040 GAGAACTGGGCGCAGACCCCAAGGTCAGGCTGCCCTGTCACTGAGCCAGGAAATCCAG 1099
QY 1081 AGATGAGAGGCGCTGAGCGAGAGAGAGGCTGTCAATCCCGAGCGAGAGAGAGAGAGC 1140
Db 1100 AGATGAGAGGCGCTGAGCGAGAGAGAGGCTGTCAATCCCGAGCGAGAGAGAGAGAGC 1159
QY 1141 AAGCTGCCGCGGAGAGGAG 1200
Db 1160 AAGCTGCCGCGGAGAGGAG 1219
QY 1201 ATGAAATGAAGCAGAGATCTGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
Db 1220 ATGAAATGAAGCAGAGATCTGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1279
QY 1261 ACATAGATGTTTTAATGTTGAAGATCAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
Db 1280 ACATAGATGTTTTAATGTTGAAGATCAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 1339
QY 1321 GTGAAAGCGGAGATCATACACTCTGAATTTGAATTTAGTATGCACATTTGTGAGGAA 1380
Db 1340 GTGAAAGCGGAGATCATACACTCTGAATTTGAATTTAGTATGCACATTTGTGAGGAA 1399
QY 1381 GAAGAGATGATTTAAATGTTTATGAGGAGCTGAATATGAAATGTAATGTAATGTA 1440
Db 1400 GAAGAGATGATTTAAATGTTTATGAGGAGCTGAATATGAAATGTAATGTAATGTA 1459
QY 1441 ATAAATGATGATCTGAGAGATGATTTATTTGAAATTTAGTATGCACATTTGTGAGGAA 1500
Db 1460 ATAAATGATGATCTGAGAGATGATTTATTTGAAATTTAGTATGCACATTTGTGAGGAA 1519
QY 1501 AAATGGAATGCTTTTAAACAGCTTTTGGGAGGCTTTGGAAGTGTCTAATAAGGTG 1560
Db 1520 AAATGGAATGCTTTTAAACAGCTTTTGGGAGGCTTTGGAAGTGTCTAATAAGGTG 1579
QY 1561 TCAAAATTTTGGTAGTAGGTATTTTGGTAGAGAGCTCAACCAAAACTGGAACATAGTT 1620
Db 1580 TCAAAATTTTGGTAGTAGGTATTTTGGTAGAGAGCTCAACCAAAACTGGAACATAGTT 1639
QY 1621 CTCTCTGAGTGTGGCAGAGCGGCGCTTCTGATCTGGAATATACCTTTGTGTAAT 1680
Db 1640 CTCTCTGAGTGTGGCAGAGCGGCGCTTCTGATCTGGAATATACCTTTGTGTAAT 1699
QY 1681 TAACAGCCACCTATAGAGAGTCCATCTGCTGTGAAGAGAGAGAGAGAGAGAGAGAG 1740
Db 1700 TAACAGCCACCTATAGAGAGTCCATCTGCTGTGAAGAGAGAGAGAGAGAGAGAGAG 1759
QY 1741 CGTGTCTGTCCAGCTGCTGTACCAAGTGTGTGCGAGCGCTGTACCTGTCTCACTG 1800
Db 1760 CGTGTCTGTCCAGCTGCTGTACCAAGTGTGTGCGAGCGCTGTACCTGTCTCACTG 1819
QY 1801 AAAGTCTGGCTAATCTCTTGTAGTCACTTCTGATCTGCAATCAATCAATCAATG 1860
Db 1820 AAAGTCTGGCTAATCTCTTGTAGTCACTTCTGATCTGCAATCAATCAATCAATG 1879
QY 1861 GCCTAGAGCACTGACTGTTAAACAAAGCTCACTAGCAAGTGAACAGCTTTAAGTCT 1920

Db 1880 GCTTAGAGCACTGACTGTTTAAACACAAAGTCACTAGCAAAAGTAGCAACAGCTTTAAGCTT 1939
QY 1921 AAATACAAAGCTGTTCTGTGTGAGAAATTTTAAAGGCTACTTGTATATTAATTAACCCCTTGT 1980
Db 1940 AAATACAAAGCTGTTCTGTGTGAGAAATTTTAAAGGCTACTTGTATATTAATTAACCCCTTGT 1999
QY 1981 CATTTTAAATGTACAAAGCGCTAATTAAGTGGCTTAGAATTTGAACATTTTGGGCTTTAT 2040
Db 2000 CATTTTAAATGTACAAAGCGCTAATTAAGTGGCTTAGAATTTGAACATTTTGGGCTTTAT 2059
QY 2041 TACTTTTCTGCTGTGTGGCAAGCAACATCTTCCCTAATATATATATTAATTAACAGAAATA 2100
Db 2060 TACTTTTCTGCTGTGTGGCAAGCAACATCTTCCCTAATATATATATTAATTAACAGAAATA 2119
QY 2101 GCAAGACGAGATAGGTTTTTGAACAAACAAACAGGCCAAAGGGGGCTGACCTGGAGC 2160
Db 2120 GCAAGACGAGATAGGTTTTTGAACAAACAAACAGGCCAAAGGGGGCTGACCTGGAGC 2179
QY 2161 AGAGCATGGTGAGGCAAGGCATGAGAGGCGAAGTTTTGTGTGGACAGATCTGTGGCT 2220
Db 2180 AGAGCATGGTGAGGCAAGGCATGAGAGGCGAAGTTTTGTGTGGACAGATCTGTGGCT 2238
QY 2221 ACTTTATTTACTGGAGTAAAGAAACAAAGTTCATTCATGTCGAAGGATATATACAGTGT 2280
Db 2239 ACTTTATTTACTGGAGTAAAGAAACAAAGTTCATTCATGTCGAAGGATATATACAGTGT 2298
QY 2281 TAGAATTTAGGATGTTTGAACAAACAGGAATACATGTTTGTATCATAGTGTACA 2340
Db 2299 TAGAATTTAGGATGTTTGAACAAACAGGAATACATGTTTGTATCATAGTGTACA 2358
QY 2341 CATTTAGCTTGTGGTAAATGACTCACAAACAGTATTTAAATCAAGTTAAATGTCAATTT 2400
Db 2359 CATTTAGCTTGTGGTAAATGACTCACAAACAGTATTTAAATCAAGTTAAATGTCAATTT 2418
QY 2401 TGAATTTACTGACTTAATCCTAATCACAAATACAAATGCGCATTAAGTGTGACCTGAGTT 2460
Db 2419 TGAATTTACTGACTTAATCCTAATCACAAATACAAATGCGCATTAAGTGTGACCTGAGTT 2478
QY 2461 GGTTCCTTAGTATTAATTTATGTAATAGGCTCTTACACATTTGCAATTAACCTGCCACATC 2520
Db 2479 GGTTCCTTAGTATTAATTTATGTAATAGGCTCTTACACATTTGCAATTAACCTGCCACATC 2538
QY 2521 ATTAATGACTGACTTCCAGTAAGGCTCTTAAGGGTAAAGTAGGAGGATCCACAGGATT 2580
Db 2539 ATTAATGACTGACTTCCAGTAAGGCTCTTAAGGGTAAAGTAGGAGGATCCACAGGATT 2598
QY 2581 TGAGATGCTAAGGCCCCAGAGATCGTTTGAACCAACCTCTTATTTTACAGAGGGGAAAT 2640
Db 2599 TGAGATGCTAAGGCCCCAGAGATCGTTTGAACCAACCTCTTATTTTACAGAGGGGAAAT 2658
QY 2641 GGGGCGCTTAGAAGTTACAGAGCATCTAGCTGGTGGCGACCCCTGGGCTCACACAGAC 2700
Db 2659 GGGGCGCTTAGAAGTTACAGAGCATCTAGCTGGTGGCGACCCCTGGGCTCACACAGAC 2718
QY 2701 TCCGAGTACTGGGACTACAGGACACAGTCACTGAAGCAGGGCGCTGTTGCAATTCAC 2760
Db 2719 TCCGAGTACTGGGACTACAGGACACAGTCACTGAAGCAGGGCGCTGTTGCAATTCAC 2778
QY 2761 GCTGCCACCTCCAACTTAAACATTTCTCATATGTGATGCTTAGTCACTAAGGTTAAAC 2820
Db 2779 GTTGCCACCTCCAACTTAAACATTTCTCATATGTGATGCTTAGTCACTAAGGTTAAAC 2838
QY 2821 TTTCOCACCCGAGAAAGGCACTTAGATAAAATCTTAGAGTACTTTCATCTTCTAAG 2880

Db 2839 TTTCOCACCCGAGAAAGGCACTTAGATAAAATCTTAGAGTACTTTCATCTCTTAAG 2898
QY 2881 TCCCTTCCAGGCTCACTTTTGAATCCTCCTTGGGTTGATAGGAATTTCTCTTGTCTTC 2940
Db 2899 TCCCTTCCAGGCTCACTTTTGAATCCTCCTTGGGTTGATAGGAATTTCTCTTGTCTTC 2958
QY 2941 TCAATAAAGTCTCATTCATCTCATGTTTAAATTTGTACGCTAGAAATTCCTGAGAATAA 3000
Db 2959 TCAATAAAGTCTCATTCATCTCATGTTTAAATTTGTACGCTAGAAATTCCTGAGAATAA 3018
QY 3001 AATGTTCTGTTCACCTT 3017
Db 3019 AATGTTCTGTTCACCTT 3035
RESULT 4
ID ABV25476
ID ABV25476 standard; cDNA; 3210 BP.
XX AC ABV25476;
XX 16-SEP-2002 (first entry)
XX Human prostate expression marker cDNA 25467.
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX Homo sapiens.
XX WO200160860-A2.
XX EN 23-AUG-2001.
XX PD 20-FEB-2001; 2001WO-US005171.
XX PF 17-FEB-2000; 2000US-0183319P.
XX PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX Novel isolated nucleic acid molecule associated with cancerous state of
prostate cells and correlating with presence of prostate cancer, useful
for detecting presence of prostate cancer, stage of prostate cancer.
XX Claim 1; Page 5059-5060; 11750pp; English.
XX The invention relates to an isolated nucleic acid molecule (I) comprising
a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
specification or its complement. (I) is useful for: (a) assessing whether
a patient is afflicted with prostate cancer; (b) monitoring the
progression of prostate cancer in a patient; (c) assessing the efficacy
of a test compound to inhibit prostate cancer in a patient; (d) assessing
the efficacy of a therapy for inhibiting prostate cancer in a patient;

(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound; (g)
determining whether prostate cancer has metastasized in a patient; (h)
assessing the aggressiveness or incidence of prostate cancer in a patient
; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
Sequence 3210 BP: 926 A; 701 C; 856 G; 717 T; 0 U; 10 Other;

[illegible][illegible]

Db 1813 TAAAGCAGCACTATAGAAGAGTCCATCTGCTGTGAAGGAGAGACAGAGAACTCTGGCTC 1872

QY 1741 CGTCTGCTCTCCAGCTGCTGTACCAAGTGGTGGTGCAGAGCTGTACCTGTTCTCACTG 1800

Db 1873 CGTCTGCTCTCCAGCTGCTGTACCAAGTGGTGGTGCAGAGCTGTACCTGTTCTCACTG 1932

QY 1801 AAAATCTGGGTAACTCTCTGTTGTGTAGTCACTCTGATCTGCAATCAATCAATCAATG 1860

Db 1933 AAAAGTCTGGTAACTCTCTGTTGTGTAGTCACTCTGATCTGCAATCAATCAATCAATG 1992

QY 1961 GCTTAGAGCACTGACTGTGTATACACAAAGTCACTAGCAAGTGAACAGCTTTAAAGTCT 1920

Db 1993 GCTTAGAGCACTGACTGTGTATACACAAAGTCACTAGCAAGTGAACAGCTTTAAAGTCT 2052

QY 1921 AAATACAAAGCTGTTCTGTGTGAGAAATTTTTAAAGGCTACTTGTATATAAACCTTGT 1980

Db 2053 AAATACAAAGCTGTTCTGTGTGAGAAATTTTTAAAGGCTACTTGTATATAAACCTTGT 2112

QY 1981 CATTTTTAAAGTCAAAAGGCTATTAAGTGGCTTAGAAATTTGAACATTTGGTCTTTAT 2040

Db 2113 CATTTTTAAAGTCAAAAGGCTATTAAGTGGCTTAGAAATTTGAACATTTGGTCTTTAT 2172

QY 2041 TTAATTTGCTTGTGTGGGCAAGCAATCTTCCCTAAATATATATATACCAAGAAA 2100

Db 2173 TTAATTTGCTTGTGTGGGCAAGCAATCTTCCCTAAATATATATATACCAAGAAA 2232

QY 2101 GCAAGAGCAGATTAAGTTTTTGACAAAACAAAGGCCAAAGGGGGCTGACCTGGAGC 2160

Db 2233 GCAAGAGCAGATTAAGTTTTTGACAAAACAAAGGCCAAAGGGGGCTGACCTGGAGC 2292

QY 2161 AGAGCATGGTGAAGGCAAGGCTAGAGGSCAGTTTGTGTGACAGATCTGTGCT 2220

Db 2293 AGAGCATGGTGAAGGCAAGGCTAGAGGSCAG- TTGTGTGACAGATCTGTGCT 2351

QY 2221 ACTTTATTAAGTGAAGGCAAGGCTAGAGGSCAGTTTGTGTGACAGATCTGTGCT 2280

Db 2352 ACTTTATTAAGTGAAGGCAAGGCTAGAGGSCAGTTTGTGTGACAGATCTGTGCT 2411

QY 2281 TAGAAATTAAGGCTGTTTAGAAAACAGGAATACATGGTGTGTTTATCATAGTGTACA 2340

Db 2412 TAGAAATTAAGGCTGTTTAGAAAACAGGAATACATGGTGTGTTTATCATAGTGTACA 2471

QY 2341 CATTTAGCTTTGGTAAATGACTCACAAGCTGATTTTAAATCAAGTTAAATGTAATTT 2400

Db 2472 CATTTAGCTTTGGTAAATGACTCACAAGCTGATTTTAAATCAAGTTAAATGTAATTT 2531

QY 2401 TGAATTAATTAAGTAAATCAATTAACAAATGCAATTAAGGCTTTGACTTGACTT 2460

Db 2532 TGAATTAATTAAGTAAATCAATTAACAAATGCAATTAAGGCTTTGACTTGACTT 2591

QY 2461 GGTCTTATTAATTAAGTAAATGAGGCTCTTACCACTTGCATAATTAAGTGGCCACATC 2520

Db 2592 GGTCTTATTAATTAAGTAAATGAGGCTCTTACCACTTGCATAATTAAGTGGCCACATC 2651

QY 2521 ATTAATTAAGTAAATGAGGCTCTTACCACTTGCATAATTAAGTGGCCACATC 2580

Db 2652 ATTAATTAAGTAAATGAGGCTCTTACCACTTGCATAATTAAGTGGCCACATC 2711

QY 2581 TGAGATGCTTAAAGGCCCAAGAGATCGTTTGAACCAACCTCTTATTTTCAAGGGGAAAAAT 2640

Db 2712 TGAGATGCTTAAAGGCCCAAGAGATCGTTTGAACCAACCTCTTATTTTCAAGGGGAAAAAT 2771

QY 2641 GGGGCTTAGAAGTTACAGAGCATCTAGCTGGTGGCTGGCAAGCTGGCTCACAAGAC 2700

Db 2772 GGGGCTTAGAAGTTACAGAGCATCTAGCTGGTGGCTGGCAAGCTGGCTCACAAGAC 2831

QY 2701 TCCGAGTAGCTGGGACTACAGGCAACAGTCACTGAAGCAGGCGCTGTTGCAATTCAC 2760

Db 2832 TCCGAGTAGCTGGGACTACAGGCAACAGTCACTGAAGCAGGCGCTGTTGCAATTCAC 2891

QY 2761 GCTGGCAGCTCCAACTTAAACATCTTCAATATGATGTCTTAGTCACTAAGGTAAAC 2820

Db 2892 GTTGGCACTCCAACTTAAACATCTTCAATATGATGTCTTAGTCACTAAGGTAAAC 2951

QY 2821 TTTCCCAAGCAGAAAGGCAACTTAGATAAAATCTTAGAGTACTTTCATCTCTTAAG 2880

Db 2952 TTTCCCAAGCAGAAAGGCAACTTAGATAAAATCTTAGAGTACTTTCATCTCTTAAG 3011

QY 2881 TCCCTTTCCAGGCTCACTTTGAGTCTCTCTTGGGCTGATAGGAATTTCTCTTGGCTTC 2940

Db 3012 TCCCTTTCCAGGCTCACTTTGAGTCTCTCTTGGGCTGATAGGAATTTCTCTTGGCTTC 3071

QY 2941 TCAATTAAGTCTCTTATTCATCTCATGTTTAAATTTGAGCAATAGTTCAGAAATAA 3000

Db 3072 TCAATTAAGTCTCTTATTCATCTCATGTTTAAATTTGAGCAATAGTTCAGAAATAA 3131

QY 3001 AATGTTCTGTTCAACTT 3017

Db 3132 AATGTTCTGTTCAACTT 3148

RESULT 5

AAHL4672

ID AAHL4672 standard; cDNA; 3045 BP.

XX AC AAHL4672;

XX DT 26-JUN-2001 (first entry)

XX DE Human cDNA sequence SEQ ID NO:12356.

XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX OS Homo sapiens.

XX PN EP1074617-A2.

XX PD 07-FEB-2001.

XX PF 28-JUL-2000; 2000EP-00116126.

XX PR 29-JUL-1999; 99JP-00248036.

PR 27-AUG-1999; 99JP-00300253.

PR 11-JAN-2000; 2000JP-00118776.

PR 02-MAR-2000; 2000JP-00183767.

PR 09-JUN-2000; 2000JP-00241899.

XX (HELI-) HELIX RES INST.

XX Ota T, Isegai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or

diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

Claim B: SEQ ID NO 12356: 2537pp + Sequence Listing; English.

The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-d^r primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and cDNAs easily without any specialised methods. AAH03166 to AAH95193, AAH13633 to AAH16742 represent human cDNA sequences; AAH92446 to AAH95193 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

Sequence 3045 BP; 895 A; 642 C; 813 G; 695 T; 0 U; 0 Other;

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every Match      99.3%; Score 2997; DB 4; Length 3045;
1st Local Similarity 99.8%; Pred. No. 0;
Matches 3011; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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[illegible]

QY 1381 GAAGAGATGATCTTAAATGTTCTATGAGGAGCTGAATAGTGAATCTGTAATGTTACTA 1440
Db 1410 GAAGAGATGATCTTAAATGTTCTATGAGGAGCTGAATAGTGAATCTGTAATGTTACTA 1469
QY 1441 AATAAATGTACATCTGAGAGATGATTAATGTGAATTTTATGATGACACTTTTGTAGGAA 1500
Db 1470 AATAAATGTACATCTGAGAGATGATTAATGTGAATTTTATGATGACACTTTTGTAGGAA 1529
QY 1501 AATATGGAATGGTCTTTTAAACAGCTTTTGGGGGGTACTTTGGAAAGTGTCTAATAAGGTT 1560
Db 1530 AATATGGAATGGTCTTTTAAACAGCTTTTGGGGGGTACTTTGGAAAGTGTCTAATAAGGTT 1589
QY 1561 TCACAAATTTTGTAGTAGTATTTCTGTGAGAGCTCAACACCAAACTGGAACATAGTT 1620
Db 1590 TCACAAATTTTGTAGTAGTATTTCTGTGAGAGCTCAACACCAAACTGGAACATAGTT 1649
QY 1621 CTCTCTCAAGTGTGTGACAGAGGGGCTTCTGTATCTGGAATATTAACCTTTGTGTAAT 1680
Db 1650 CTCTCTCAAGTGTGTGACAGAGGGGCTTCTGTATCTGGAATATTAACCTTTGTGTAAT 1709
QY 1681 TAACAGCCACCTATAGAGAGTCCATCTGCTGTGAAGGAGAGACAGAGAACTCTGGGTTTC 1740
Db 1710 TAACAGCCACCTATAGAGAGTCCATCTGCTGTGAAGGAGAGACAGAGAACTCTGGGTTTC 1769
QY 1741 CGTGTCTCTGTCACAGTGTCTGTACCAAGTGTCTGTGTCAGAGCTGTACCTGTTCTCACTG 1800
Db 1770 CGTGTCTCTGTCACAGTGTCTGTACCAAGTGTCTGTGTCAGAGCTGTACCTGTTCTCACTG 1829
QY 1801 AAAAGTCTGGCTAATGCTCTGTGTAGTCACTTTCTGATCTGACAACTCAATCAATG 1860
Db 1830 AAAAGTCTGGCTAATGCTCTGTGTAGTCACTTTCTGATCTGACAACTCAATCAATG 1889
QY 1861 GCTTAGAGACTGACTGTTTAACACAAAGCTCACTAGCAAGTAGACAGAACTTTAAGTCT 1920
Db 1890 GCTTAGAGACTGACTGTTTAACACAAAGCTCACTAGCAAGTAGACAGAACTTTAAGTCT 1949
QY 1921 AATACAAAGCTGTTCTGTGTGAGAAATTTTAAAGGCTACTTGTATATACCCCTGT 1980
Db 1950 AATACAAAGCTGTTCTGTGTGAGAAATTTTAAAGGCTACTTGTATATACCCCTGT 2009
QY 1981 CATTTTAAATGTACAAAGCTATTAAAGTGGCTTAGAAATTTGAACATTTGTGGCTTTAT 2040
Db 2010 CATTTTAAATGTACAAAGCTATTAAAGTGGCTTAGAAATTTGAACATTTGTGGCTTTAT 2069
QY 2041 TTACTTTGCTTGTGTGGGCAAGCAACATCTTCCCTTAATATATATTACCAAGAAA 2100
Db 2070 TTACTTTGCTTGTGTGGGCAAGCAACATCTTCCCTTAATATATATTACCAAGAAA 2129
QY 2101 GCAAGAGCAAGTTAGTGTGTTTGAACAAACAAAGGCAAGGAGGCTGACCTGGAGC 2160
Db 2130 GCAAGAGCAAGTTAGTGTGTTTGAACAAACAAAGGCAAGGAGGCTGACCTGGAGC 2189
QY 2161 AGAGCATGTTGAGAGGCAAGGCAATGAGAGGCAAGTTTTGTGTGGACAGATCTGTGCT 2220
Db 2190 AGAGCATGTTGAGAGGCAAGGCAATGAGAGGCAAGT-TTTGTGTGGACAGATCTGTGCT 2248
QY 2221 ACTTTATCTGGAGTAAAGAAACAAAGTTCATTGATGTCCAGAGATATATACAGTGT 2280
Db 2249 ACTTTATCTGGAGTAAAGAAACAAAGTTCATTGATGTCCAGAGATATATACAGTGT 2308
QY 2281 TAGAAATTAGGACTGTTTGAAGAAACAGGAAATACATGTTGTTTTATCATAGTGTACA 2340
Db 2309 TAGAAATTAGGACTGTTTGAAGAAACAGGAAATACATGTTGTTTTATCATAGTGTACA 2368

QY 2341 CATTTAGCTTGTGTTAAATGACTCACAATACTGATTTTAAATCAAGTAAATGTAATTT 2400
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Db 2429 TGAATAATTAAGTAAATGCTAAATTCACAAATGCAATTAAGGTTTGAAGTGTGACTT 2488
QY 2461 GGTTCCTAGTAAATATATGATGATTAAGTGTGCTTACCACTTGCMAATTAAGTGTGCTT 2520
Db 2489 GGTTCCTAGTAAATATATGATGATTAAGTGTGCTTACCACTTGCMAATTAAGTGTGCTT 2548
QY 2521 ATTAATGACTGACTTCCCAAGTAAAGGCTCTCTAAGGGGTAAGTAGAGGATCCACAGAT 2580
Db 2549 ATTAATGACTGACTTCCCAAGTAAAGGCTCTCTAAGGGGTAAGTAGAGGATCCACAGAT 2608
QY 2581 TGAGATGCTAAGGCCCCAGAGATCGTTTGAACCAACCTCTTATTTTCAGAGGGGAAAT 2640
Db 2609 TGAGATGCTAAGGCCCCAGAGATCGTTTGAATCCACCTCTTATTTTCAGAGGGGAAAT 2668
QY 2641 GGGGCTTAGAAGTTACAGAGATCTAGCTGGTGGCTGGCAAGCTTGGCTTCAACAGAC 2700
Db 2669 GGGGCTTAGAAGTTACAGAGATCTAGCTGGTGGCTGGCAAGCTTGGCTTCAACAGAC 2728
QY 2701 TCCGAGTAGCTGGGACTACAGGACACACAGTCACTGAGCAGGCGCTGTTGCAATTCAC 2760
Db 2729 TCCGAGTAGCTGGGACTACAGGACACACAGTCACTGAGCAGGCGCTGTTGCAATTCAC 2788
QY 2761 GCTGCGACCTCCAACTTAAACATTTCTCATATGATGTCTTATGATGATGATGATGATGAT 2820
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QY 2881 TCTCTTCCAGCTCAGCTTTCAGTCTCTCTGCTGGGTTGATAGGAATTTTCTCTGCTTTC 2940
Db 2909 TCTCTTCCAGCTCAGCTTTCAGTCTCTCTGCTGGGTTGATAGGAATTTTCTCTGCTTTC 2968
QY 2941 TCATAAAGTCTCTATTCATCTCATGTTTAAATTTGAAGTGTGATGATGATGATGATGATGAT 3000
Db 2969 TCATAAAGTCTCTATTCATCTCATGTTTAAATTTGATAGGATTTTCTCTGCTTTC 3028
QY 3001 AATGTTCTGTTCACTT 3017
Db 3029 AATGTTCTGTTCACTT 3045

RESULT 6
ID ACC50169 standard; cDNA; 3042 bp.
AC ACC50169;
XX
XX 12-JUN-2003 (first entry)
XX
XX Breast cancer associated cDNA sequence SEQ ID NO:183.
XX Human; breast cancer; cytostatic; gene therapy; gene; ss.
XX Homo sapiens.

XX
FN WC200304989-A2.
XX
PD 16-JUN-2003.
XX
PF 21-JUN-2002; 2002WO-US019669.
XX
PR 21-JUN-2001; 2001US-0299887P.
PR 27-JUN-2001; 2001US-0301572P.
PR 18-JUL-2001; 2001US-0306501P.
PR 25-SEP-2001; 2001US-0325002P.
PR 05-MAR-2002; 2002US-0362585P.
PR 14-MAY-2002; 2002US-0380391P.
XX
PA (MILL-) MILLENIUM PHARM INC.
XX
PI Lillie J, Gannavarapu M, Glatt K, Hoersh S, Kamatkar S;
PI Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;
PI Bast RC, Hortobagyi GN, Fuzstai L, Meric F, Sahin A, Mills SB;
XX
XX WPI; 2003-210381/20.
DR P-PSDB; AB347475.
XX
XX Breast cancer diagnosis or treatment by comparing the level of expression
PT of a marker in a patient sample with that in the control non-breast
PT cancer sample.
XX
XX Claim 1; SEQ ID NO 183; 128pp; English.
XX
XX The present invention describes a method for assessing whether a patient
CC is afflicted with breast cancer. The method comprises comparing the level
CC of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and
CC ABR47386 to ABR47632) in a patient sample and the normal level of
CC expression of the marker in a control non-breast cancer sample, where a
CC significant increase in the level of expression of the marker in the
CC patient sample and the normal level is an indication that the patient is
CC afflicted with breast cancer. The breast cancer associated sequences from
CC the present invention have cytostatic activities and can be used in gene
CC therapy. The method is useful for diagnosing and treating breast cancer.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 3042 BP; 910 A; 635 C; 802 G; 695 T; 0 U; 0 Other;
Query Match 99.0%; Score 2987.6; DB 7; Length 3042;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 3012; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
QY 1 GCTGGCGGCA CGGCGGAGCGCGCGCGGAGCTCGAGCGCGCGCGCGCGCGGCGGCGGAGCGACC 60
DB 1 GCTGGCGGCA CGGCGGAGCGCGCGCGGAGCTCGAGCGCGCGCGCGCGCGGCGGCGGAGCGACC 67
QY 61 CGGCGGCGCTGCTAGCGGCGCGCGGATCCCGAGTGGCGCGCGCGGAGCGCTCGGAAAGAGA 120
DB 68 CGGCGGCGCTGCTAGCGGCGCGCGGATCCCGAGTGGCGCGCGCGGAGCGCTCGGAAAGAGA 127
QY 121 TTCTCAGCGCTGATTTTGATGATGATGGGCTTGGGAAAGCGGCGCTCGGAGCATGAGTGGC 180
DB 128 TTCTCAGCGCTGATTTTGATGATGATGGGCTTGGGAAAGCGGCGCTCGGAGCATGAGTGGC 187
QY 181 CGCCCTCTGCTGGCGCGCTGGTGGCTGGCATCATGCTCTGGGCTCTCACTACTGGA 240
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DB 188 CGCCCTCTGCTGGCGCGCTGGTGGCTTGGCATCATGCTCTTGGGCTTCACTACTGGA 247
QY 241 TTGGGAGCTCCCGGAGCGGTGGACCTCCAGACACGCGATCATGAGCTGGAGGAGGCTCC 300
DB 248 TTGGGAGCTCCCGGAGCGGTGGACCTCCAGACACGCGATCATGAGCTGGAGGAGGCTCC 307
QY 301 CGAGGCGGCTGCGAGAGAGGCGCGGTGGAGCTGAGAGAGAAAGAGTTCAGGGAGAGC 360
DB 308 GCGAGGCGGCTGCGAGAGAGGCGCGGTGGAGCTGAGAGAGAAAGAGTTCAGGGAGAGC 367
QY 361 TGGAGAGAGAGCGGGGAGCGGCTTGACAAATCCAGTCCAGCGACAACTTCCAGCTGGAGC 420
DB 368 TGGAGAGAGAGCGGGGAGCGGCTTGACAAATCCAGTCCAGCGACAACTTCCAGCTGGAGC 427
QY 421 CGCTCAACAGCTGTACAGGCGGAGGCGGTGGTGAATTAACATCAACACAGGTG 480
DB 428 CGCTCAACAGCTGTACAGGCGGAGGCGGTGGTGAATTAACATCAACAGGTG 487
QY 481 AGAGGCTCATCCGAGTGTGCAAGAGCGGTTAAAGACCTTGCAGAGGAAATACGGCAGCG 540
DB 488 AGAGGCTCATCCGAGTGTGCAAGAGCGGTTAAAGACCTTGCAGAGGAAATACGGCAGCG 547
QY 541 TCGAGCGAGTGTCTCTCCAGTTTCAAGAGAAACAGACCACTGGAGAGGAGTTCTCT 600
DB 548 TCGAGCGAGTGTCTCTCCAGTTTCAAGAGAAACAGACCACTGGAGAGGAGTTCTCT 607
QY 601 AGGACCTGAGCGAGTGCATCAATCAGATGAGGAGGTGAGGAAACAGTGTGAGGAGGAA 660
DB 608 AGGACCTGAGCGAGTGCATCAATCAGATGAGGAGGTGAGGAAACAGTGTGAGGAGGAA 667
QY 661 TAGAAGAGTCAACAAAAAGGGGATGAAGCTGTAGCTTCCAGAGACCTGAGTGAAGAA 720
DB 668 TAGAAGAGTCAACAAAAAGGGGATGAAGCTGTAGCTTCCAGAGACCTGAGTGAAGAA 727
QY 721 AGGACAGAGACAGCGCTCCAGGCGCTCAGTGTAGGCTCAGGCCAGGCCAGGCGAGG 780
DB 728 AGGACAGAGACAGCGCTCCAGGCGCTCAGTGTAGGCTCAGGCCAGGCCAGGCGAGG 787
QY 781 GCTGCGACACACAGAGTGCACAGGAGGAAAGGAAAGCTGCTTGGTAAACAGCAAGTCCC 840
DB 788 GCTGCGACACACAGAGTGCACAGGAGGAAAGGAAAGCTGCTTGGTAAACAGCAAGTCCC 847
QY 841 AGACACAGGCGCGCGGCTCCGAGTGGTGGATTCGAGTTCGAGGAGCAAGTGGAGAGG 900
DB 848 AGACACAGGCGCGCGGCTCCGAGTGGTGGATTCGAGTTCGAGGAGCAAGTGGAGAGG 907
QY 901 AAACCAATGAGTCCAGTGGTGAAGAGAGCTGAGAGGAGCGCTCAGAGGAGCGCTTCCGGGAGGAGC 960
DB 908 AAACCAATGAGTCCAGTGGTGAAGAGAGCTGAGAGGAGCGCTCAGAGGAGCGCTTCCGGGAGGAGC 967
QY 961 CAGGCGGAGAGCGGCTGGAGAGAGAGCTGTAGTGGAGAGAGGCTTCCGGGAGGAGC 1020
DB 968 CAGGCGGAGAGCGGCTGGAGAGAGAGCTGTAGTGGAGAGAGGCTTCCGGGAGGAGC 1027
QY 1021 GAGAACTGGGCGACACCGCCAGAGTGCAGGCTGGCGCTGTGAGTGGAGCGGAGGAGGAGG 1080
DB 1028 GAGAACTGGGCGACACCGCCAGAGTGCAGGCTGGCGCTGTGAGTGGAGCGGAGGAGGAGG 1087
QY 1081 AGATGAGGCGCTGAGCGAGACCGAGTGTATCCCGGAGCGGAGGAGGAGGAGGAGG 1140
DB 1088 AGATGAGGCGCTGAGCGAGACCGAGTGTATCCCGGAGCGGAGGAGGAGGAGGAGG 1147
QY 1141 AAGTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200

Db 1148 AAGCTGCGGGGAGAGGAGAGAAACAGCAGAGAACTGAGAGGAGAGAGAGTGCATCAACATGG 1207
Qy 1201 ATGAAATGAGCAGAGATCTGAGCAGAGCAAGCAGCCCTGGCAGGAGATGACAGAA 1260
Db 1208 ATGAAATGAGCAGAGATCTGAGCAGAGCAAGCAGCCCTGGCAGGAGATGACAGAA 1267
Qy 1261 ACATAGATGTTTTTAAATGTTGAAGATCAGAAAGAGACACCATAAATTTACTTGTATCAGC 1320
Db 1268 ACATAGATGTTTTTAAATGTTGAAGATCAGAAAGAGACACCATAAATTTACTTGTATCAGC 1327
Qy 1321 GTGAAACCGGAGATCATACACTCTGAATTTGAATCGAATTCACATATTTCAAGACGGGOC 1380
Db 1328 GTGAAACCGGAGATCATACACTCTGAATTTGAATCGAATTCACATATTTCAAGACGGGOC 1387
Qy 1391 GAGAGATGACTTTAAATGTTGATGAGGACTGAATTTGAATTTGAAATTTGAAATTTGACTA 1440
Db 1398 GAGAGATGACTTTAAATGTTGATGAGGACTGAATTTGAAATTTGAAATTTGACTA 1447
Qy 1441 AATAAATGTACATCTGAAGATGATTTATGTGAATTTTATGATGACTTTGTAGGAA 1500
Db 1448 AATAAATGTACATCTGAAGATGATTTATGTGAATTTTATGATGACTTTGTAGGAA 1507
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Db 1508 AAATGGATGGTCTTTAAACAGCTTTTGGGGGGTACTTTGGAGTGTCTAATAGGT 1567
Qy 1560 GTCAACATTTTGTAGTGTATTTGAGAGCTCAACACCAAACTGGACATAGT 1619
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Qy 1620 TCTCCTCAAGTGTGGGACAGCGGGGCTTCCTGATTCGGAATATACCTTTGTGAAA 1679
Db 1628 TCTCCTCAAGTGTGGGACAGCGGGGCTTCCTGATTCGGAATATACCTTTGTGAAA 1687
Qy 1680 TTAACAGCCACTATAGAGAGTCCATCTGCTGTGAAGGAGACAGAGACTCTGGGTT 1739
Db 1688 TTAACAGCCACTATAGAGAGTCCATCTGCTGTGAAGGAGACAGAGACTCTGGGTT 1747
Qy 1740 CCGTCTCTCTCCACGTGCTGTACCAAGTGTGCTGCCAGGCTTTTAOCTGTTCTCACT 1799
Db 1748 CCGTCTCTCTCCACGTGCTGTACCAAGTGTGCTGCCAGGCTTTTAOCTGTTCTCACT 1807
Qy 1800 GAAAGCTGCGCTAATGCTCTTGTGTAGTCACTTCTGATTCGACATCAATCAATCAAT 1859
Db 1808 GAAAGCTGCGCTAATGCTCTTGTGTAGTCACTTCTGATTCGACATCAATCAATCAAT 1867
Qy 1860 GGCCTAGACACTGACTGTTAACACAAAGTCACTAGCAAGGTAGCAACAGCTTTAAGTC 1919
Db 1868 GGCCTAGACACTGACTGTTAACACAAAGTCACTAGCAAGGTAGCAACAGCTTTAAGTC 1927
Qy 1920 TAAATACAAAGCTGCTGCTGTGAGAAATTTTAAAGGCTAGTTGATTAATAACCCCTG 1979
Db 1928 TAAATACAAAGCTGCTGCTGTGAGAAATTTTAAAGGCTAGTTGATTAATAACCCCTG 1987
Qy 1980 TCATTTTAAATGATCAAAACGCTATTAAAGTGGCTTAGATTTGACATTTTGGTCTTAA 2039
Db 1988 TCATTTTAAATGATCAAAACGCTATTAAAGTGGCTTAGATTTGACATTTTGGTCTTAA 2047
Qy 2040 TTTACTTTGCTTCTGCTGTGGGCAAGCAACATCTTCCCTAAATATATATACCAAGAA 2099
Db 2048 TTTACTTTGCTTCTGCTGTGGGCAAGCAACATCTTCCCTAAATATATATATACCAAGAA 2107

Qy 2100 AGCAAGAGCAGATAGTGTITTGACAAACAAAGCCCAAAAGGGGCTGACCTGGAG 2159
Db 2108 AGCAAGAGCAGATAGTGTITTGACAAACAAAGCCCAAAAGGGGCTGACCTGGAG 2167
Qy 2160 CAGAGCATGCTGAGAGGCAAGCAGTGAAGGCAAGTGTGTGTGACAGATCTGTGGC 2219
Db 2168 CAGAGCATGCTGAGAGGCAAGCAGTGAAGGCAAGTGTGTGTGACAGATCTGTGGC 2226
Qy 2220 TACTTTTACTCTGAGTAAAGAAAAAAAGTTTCAITGTGTGAAAGATATACAGTG 2279
Db 2227 TACTTTTACTCTGAGTAAAGAAAAAAAGTTTCAITGTGTGAAAGATATACAGTG 2286
Qy 2280 TTAGAAATTAGGACTGTTTAGAAAAACAGGAATACAAATGGTGTGTGTGTATCATAGTGTAC 2339
Db 2287 TTAGAAATTAGGACTGTTTAGAAAAACAGGAATACAAATGGTGTGTGTGTATCATAGTGTAC 2346
Qy 2340 ACATTTAGCTTGTGTAAATGACTCACAAACTGATTTTAAATCAAGTTAAATGCAAT 2399
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Qy 2400 TTGAAATTTACTACTTAATCCTTAATTCACAAATCAATGGGCAATTAAGTTTGACTGTGT 2459
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Qy 2460 TGGTCTTACTTATTTATGTTAAATAGGCTCTTACCACTTGCAATTAACCTGGCCACAT 2519
Db 2467 TGGTCTTACTTATTTATGTTAAATAGGCTCTTACCACTTGCAATTAACCTGGCCACAT 2526
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Db 2527 CATTAATGACTGACTTCCACTAAGGCTCTCTAAGGGGTAAAGTGGAGATCCAGAGAT 2586
Qy 2580 TTGAGATGCTAAGGCCCCAGATCGTTTGAACCAACCTCTTATTTTCAAGGGGAAAA 2639
Db 2587 TTGAGATGCTAAGGCCCCAGATCGTTTGAACCAACCTCTTATTTTCAAGGGGAAAA 2646
Qy 2640 TGGGGCTTAGAGTTACAGAGCATCTAGCTGTGCTGGCACCCCTGGCTCACACAGA 2699
Db 2647 TGGGGCTTAGAGTTACAGAGCATCTAGCTGTGCTGGCACCCCTGGCTCACACAGA 2706
Qy 2700 CTCOCGAGTAGCTGGGACTACAGGCACAGTCACTGAAGCAGGCGCTGTTTGCAATCA 2759
Db 2707 CTCOCGAGTAGCTGGGACTACAGGCACAGTCACTGAAGCAGGCGCTGTTTGCAATCA 2766
Qy 2760 GGTGGCACCTCCACTTAACATCTTCCATATGTGATGTCTTAGTCACTAAGGTTAA 2819
Db 2767 GGTGGCACCTCCACTTAACATCTTCCATATGTGATGTCTTAGTCACTAAGGTTAA 2826
Qy 2820 GTTCCCAACCCAGAAAGGCACTTAGATAAAATCTTAGAGTACTTTTCACTCTCTAA 2879
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Qy 2880 GTCTCTTCCAGGCTCACTTTGAGTCTCTTGGGGTTGATAGGAATTTCTCTTGTCTT 2939
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Qy 2940 CTCAATAAGTCTCTATTCATCTCATCTGTTAATTTGTAGGCAATAGATTCCTGAGAAATA 2999
Db 2947 CTCAATAAGTCTCTATTCATCTCATCTGTTAATTTGTAGGCAATAGATTCCTGAGAAATA 3006
Qy 3000 AAAATGTTCTGTTCAACTT 3017
Db 3007 AAAATGTTCTGTTCAACTT 3024

RESULT 7

ADB75331 ID ADB75331 standard; cDNA; 3042 BP.

XX AC ADB75331;
XX DT 04-DEC-2003 (first entry)
XX DE Prostate cancer marker cDNA.
XX KW Prostate; cancer; cytostatic; gene therapy; marker; ss.
XX OS Homo sapiens.

XX PN W0200309814-A2.
XX PD 06-FEB-2003.
XX PF 25-JUL-2002; 2002WO-US023913.
XX PR 25-JUL-2001; 2001US-0307982P.
XX PR 22-AUG-2001; 2001US-0314356P.
XX PR 25-SEP-2001; 2001US-032520P.
XX PR 12-DEC-2001; 2001US-0341746P.
XX PR 05-MAR-2002; 2002US-0362158P.

XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;
XX PI Hoersht S, Kamatkar S, Wonsley AM, Glatt K, Zhao X, Anderson D;
XX PR WPI; 2003-248033/24.
XX PT New nucleic acid molecule, useful for diagnosing or treating prostate cancer.
XX PS Disclosure; SEQ ID NO 155; 99pp; English.

XX CC The invention relates to newly discovered cancer markers associated with the cancerous state of prostate cells. Also disclosed is a method of assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with prostate cancer by comparing the level of expression of a marker in a patient sample and the normal level of expression of the marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal level indicates that the patient is afflicted with prostate cancer. Nucleic acids of the invention are useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequences given in ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 3042 BP; 910 A; 635 C; 802 G; 695 T; C U; 0 Other;

Query Match 99.0%; Score 2987.6; DB 9; Length 3042;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 3012; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 1 GCTGGGCGCA CGCGCGGAGAGCTCGAGGCGCGCGCGGCGGAGGCGGACC 60

DB 8 GCTGGGCGCA CGCGCGGAGAGCTCGAGGCGCGCGCGGCGGAGAGGCGACC 67
QY 61 CGGGCGGCTCGTAGCGGGGCGCGCGGATCCCGGAGTGGCGGGCGCGCGGAGAGAGAGA 120
DB 68 CGGGCGGCTCGTAGCGGGGCGCGCGGATCCCGGAGTGGCGGGCGCGCGGAGAGAGAGA 127
QY 121 TTCTCAGCGCTGATTTGATGATGGGCTTGGGAAAGGCGCTCGACGATGAAGTCGG 180
DB 128 TTCTCAGCGCTGATTTGATGATGGGCTTGGGAAAGGCGCTCGACGATGAAGTCGG 187
QY 181 CGCGCTCGTGGTGGCGCGCTGGTGGCTGATCATGCTTGGCTTCAACTACTTGA 240
DB 188 CGCGCTCGTGGTGGCGCGCTGGTGGCTGATCATGCTTGGCTTCAACTACTTGA 247
QY 241 TTGCGAGCTCCCGGAGGCTGGACCTCCAGACGCGATCATGAGCTGGAGGCGAGGTC 300
DB 248 TTGCGAGCTCCCGGAGGCTGGACCTCCAGACGCGATCATGAGCTGGAGGCGAGGTC 307
QY 301 GCAGGGGCGCTGCAGAGAGGCGCGTGGAGCTGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 308 GCAGGGGCGCTGCAGAGAGGCGCGTGGAGCTGAGAGAGAGAGAGAGAGAGAGAGAG 367
QY 361 TGGAG 420
DB 368 TGGAG 427
QY 421 GGCTCAAGAGCTGTACAG 480
DB 428 GGCTCAAGAGCTGTACAG 487
QY 481 AGAGGCTCATCGGAGTGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 486 AGAGGCTCATCGGAGTGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 547
QY 541 TGCAGAGAGAGTGTCTCCAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 548 TGCAGAGAGAGTGTCTCCAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 607
QY 601 AGAGCTGAGCGAGTGCATCATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 608 AGAGCTGAGCGAGTGCATCATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 667
QY 661 TAGAGAGAGTCAACCAAG 720
DB 668 TAGAGAGAGTCAACCAAG 727
QY 721 ACAGCAG 780
DB 728 ACAGCAG 787
QY 781 GCTTGCACACAGAGAGTGCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 788 GCTTGCACACAGAGAGTGCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 847
QY 841 AGAGCAG 900
DB 848 AGAGCAG 907
QY 901 AAGACAG 960
DB 908 AAGACAG 967

QY 961 CAGGCCGGGACGAGGTGGTGGAGACAGACCTGTAGTGGAGAGAGGCTTCGGGGGAGCG 1020
D5 968 CAGGCCGGGACGAGGTGGTGGAGACAGACCTGTAGTGGAGAGAGGCTTCGGGGGAGCG 1027
QY 1021 GAGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTCACTGAGCCAGGAAAATCCAG 1080
D5 1026 GAGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTCACTGAGCCAGGAAAATCCAG 1087
QY 1081 AGATGAGGGGCCCTGAGGAGACGACGCTGTCACTCCCGAGCGGACAGGAGGAGGAGG 1140
D5 1088 AGATGAGGGGCCCTGAGGAGACGACGCTGTCACTCCCGAGCGGACAGGAGGAGGAGG 1147
QY 1141 AAGCTGCCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
D5 1148 AAGCTGCCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1207
QY 1201 ATGAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260
D5 1208 ATGAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1267
QY 1261 ACATAGATGTTTTTAATGTTGAAGATCAGAAAAGAGACACATTAATTTACTTGTATCAG 1320
D5 1268 ACATAGATGTTTTTAATGTTGAAGATCAGAAAAGAGACACATTAATTTACTTGTATCAG 1327
QY 1321 GTGAAAGGGGATCATACACTCTGAATTCGAACTGCAATCAATATTTCAACACAGGCG 1380
D5 1328 GTGAAAGGGGATCATACACTCTGAATTCGAACTGCAATCAATATTTCAACACAGGCG 1387
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D5 1386 GAGAGATGACTTTAAATGTTTCAAGGAGGAGTGAATGAACTGAAATGAACTGAAATGAACT 1447
QY 1441 AATAAATGATCTGATGAGATGATTAATGGAATTTTGAATGCACTTTGTGATGAGAA 1500
D5 1448 AATAAATGATCTGATGAGATGATTAATGGAATTTTGAATGCACTTTGTGATGAGAA 1507
QY 1501 AATAAATGATCTGATGAGATGATTAATGGAATTTTGAATGCACTTTGTGATGAGAA 1559
D5 1508 AATAAATGATCTGATGAGATGATTAATGGAATTTTGAATGCACTTTGTGATGAGAA 1567
QY 1560 GTCAAAATTTTGGTGTAGTGGTATTTTCGTGAGAGCTCAACACCAAACTGGAACTATG 1619
D5 1568 GTCAAAATTTTGGTGTAGTGGTATTTTCGTGAGAGCTCAACACCAAACTGGAACTATG 1627
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D5 1628 TCTCCTTCAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1687
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D5 1688 TTAACAGCACTATAGAGAGTCCATCTGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 1747
QY 1740 CCGTCCTCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1799
D5 1748 CCGTCCTCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1807
QY 1800 GAAATGCTGGCTAATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1859
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D5 2287 TTAGAAATAGGACTGTTTAGAAAACAGGAAATACATGCTGTTTATCATAGTGTAC 2346
QY 2340 ACATTTAGCTGTGTGTAATGATCACAAAACGATTTTAAATCAAGTGTATGTGAAT 2399
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 Qy 2940 CTCATAAAGTCTCTATCATCTCAGTTTAAATTGACGATAGATTTGTCAGAAATA 2999
 Db 2947 CTCATAAAGTCTCTATCATCTCAGTTTAAATTGACGATAGATTTGTCAGAAATA 3006
 Qy 3000 AATGTTCTTGTTCAACTT 3017
 Db 3007 AATGTTCTTGTTCAACTT 3024
 RESULT 8
 ADD18542
 ID ADD18542 standard; DNA; 3042 BP.
 AC ADD18542;
 XX
 DT 15-JAN-2004 (first entry)
 DE Human prostate cancer: diagnosis related DNA sequence SegID114.
 KW prostate tissue; cancer diagnostic; cancer marker; prostate cancer; PCA;
 KW male cancer-related death; serum biomarker; tissue biomarker; cytostatic;
 KW gene therapy; prostate biopsy tissue; AMACR;
 KW alpha-methylacyl-coenzyme A racemase; diagnosing cancer; cell growth;
 KW human; ds.
 XX
 OS Homo sapiens.
 XX
 FN W02003012067-A2.
 PD 13-FEB-2003.
 XX
 PF C2-AUG-2002; 2002W0-US024567.
 XX
 PR 02-AUG-2001; 2001US-0309581P.
 PR 15-NOV-2001; 2001US-0334468P.
 PR 01-AUG-2002; 2002US-00210120.
 XX
 PA (UNMI) UNIV MICHIGAN.
 XX
 PI Rubin MA, Chinnaiyan AM, Sreekumar A;
 XX
 DR WPI; 2003-278396/27.
 XX
 PT Characterizing prostate tissue comprises providing a prostate tissue
 sample from a subject and detecting the presence or absence of expression
 of hepsin, pim-1 or EZH2.
 XX
 PS Disclosure; SEQ ID NO 114; 297bp; English.
 XX
 CC This invention relates to a novel method of characterising prostate
 tissue in a subject and to compositions and methods for cancer
 diagnostics, including cancer markers, in particular prostate cancer.
 CC Prostate cancer (PCA) is a leading cause of male cancer-related death.
 CC Additional serum and tissue biomarkers would aid diagnosis. The invention
 may provide means of producing compounds with a cytostatic activity or
 allow the development of gene therapy. The methods of the invention
 are useful for characterising prostate tissue in a subject, screening

CC compounds, characterising inconclusive prostate biopsy tissue in a
 subject, detecting AMACR (alpha-methylacyl-coenzyme A racemase),
 CC expression in a bodily fluid, characterising tissue in a subject,
 CC diagnosing cancer in a subject and inhibiting the growth of cells. The
 CC present sequence is a DNA sequence which is preferably utilised in the
 CC method of the invention.
 XX
 SQ Sequence 3042 BP; 910 A; 635 C; 802 G; 695 T; 0 U; 0 Other;
 Query Match 99.0%; Score 2987.6; DB 9; Length 3042;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 3012; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
 Qy 1 GCTGGGCGCAGCGGCGGAGCGGCGGCGGAGCTCGAGGCGGCGGCGGAGAGCGGACC 60
 Db 8 GCTGGGCGCAGCGGCGGAGCGGCGGAGCTCGAGGCGGCGGCGGAGAGCGGACC 67
 Qy 61 CGGGCGGCGCTCGTAGCGGGGCGGCGGATCCCGAGTGGGCGGCGGAGCTCGAAAGAGA 120
 Db 68 CGGGCGGCGCTCGTAGCGGGGCGGCGGATCCCGAGTGGGCGGCGGAGCTCGAAAGAGA 127
 Qy 121 TTCTCAGCGCTGATTTTGAGATGATGGGCTTGGGAAACGGGGCTCGCAGCATGAAGTCCG 180
 Db 128 TTCTCAGCGCTGATTTTGAGATGATGGGCTTGGGAAACGGGGCTCGCAGCATGAAGTCCG 187
 Qy 181 CGGGCGGCGCTGCTGGGCGGCGGCTGGTGGCTGCATCATCTCTTGGCTTCACTACTGGA 240
 Db 188 CGGGCGGCGCTGCTGGGCGGCGGCTGGTGGCTGCATCATCTCTTGGCTTCACTACTGGA 247
 Qy 241 TTGGAGGCTCCCGGAGCGCTGGAGCTCCAGACACGGATCATGGAGCTGGAAAGGCGAGTCC 300
 Db 248 TTGGAGGCTCCCGGAGCGCTGGAGCTCCAGACACGGATCATGGAGCTGGAAAGGCGAGTCC 307
 Qy 301 GCGGGCGGCTGGCAG 360
 Db 308 GCGGGCGGCTGGCAG 367
 Qy 361 TGGAG 420
 Db 368 TGGAG 427
 Qy 421 GGGTCAACAGCTGTACCAAG 480
 Db 428 GGGTCAACAGCTGTACCAAG 487
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 Qy 601 ACGACCTGAGCCAGTGCATCAATCAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
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 Qy 661 TAGAAGAGGTCAACAAAAG 720
 Db 668 TAGAAGAGGTCAACAAAAG 727
 Qy 721 ACGACCAAG 780

Ds 728 ACGACGACGACGACGACGCTCGAAGGCTCAGTGAGCTCAGCCCGGCTGCGAGGACGAG 787
QY 781 GCGTCCACACACACAGAGGTGACACAGGGAAGGGAAGGCTGCTTGGTAACAGCAAGTCC 840
Ds 788 GCGTCCACACACACAGAGGTGACACAGGGAAGGGAAGGCTGCTTGGTAACAGCAAGTCC 847
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Ds 908 AAACCAATGAGATCCAGTGGTGAATGAGGAGGCTCAGAGGACAGGCTGCGGACGAGC 967
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Ds 1628 TCTCCTTCAAGTGTGGGACAGCGGGGCTTCTGATTTCTGGAATATTAACCTTTGTGAAA 1687
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Ds 1808 GAAAGTCTGT 1867
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Ds 1868 GGCCTAGAGCAGT 1927
QY 1920 TAAATACAAAAGT 1979
Ds 1928 TAAATACAAAAGT 1987
QY 1980 TCAATTTTAAATGACAAAAGT 2039
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Ds 2287 TTAGAAATAGGAGT 2346
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| 6 | 2876 | 95.3 | 3174 | 12 | US-10-351-334-86 |
| 7 | 2744.8 | 91.0 | 2962 | 15 | US-10-104-047-1343 |
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| 13 | 1427.4 | 47.3 | 1429 | 12 | US-10-143-118-485 |
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| 15 | 1427.4 | 47.3 | 1429 | 12 | US-10-158-787-485 |
| 16 | 1427.4 | 47.3 | 1429 | 12 | US-10-140-024-485 |
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| 18 | 1427.4 | 47.3 | 1429 | 14 | US-10-121-049-485 |
| 19 | 1427.4 | 47.3 | 1429 | 14 | US-10-123-904-485 |
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| 21 | 1427.4 | 47.3 | 1429 | 14 | US-10-075-618-485 |
| 22 | 1427.4 | 47.3 | 1429 | 14 | US-10-076-918-485 |
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| 40 | 1427.4 | 47.3 | 1429 | 14 | US-10-140-921-485 |
| 41 | 1427.4 | 47.3 | 1429 | 14 | US-10-140-928-485 |
| 42 | 1427.4 | 47.3 | 1429 | 14 | US-10-015-393A-99 |
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| 45 | 1427.4 | 47.3 | 1429 | 14 | US-10-121-292-485 |

RESULT 1

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1  RES001 1
2  ; Sequence 1654, Application: US/10342887
3  ; Publication No. US20040058340A1
4  ; GENERAL INFORMATION:
5  ; APPLICANT: Dai, Hongyue
6  ; APPLICANT: He, Yudong
7  ; APPLICANT: Linsley, Peter S.
8  ; APPLICANT: Mao, Mao
9  ; APPLICANT: Roberts, Christopher J.
10 ; APPLICANT: Van 't Veer, Laura Johanna
11 ; APPLICANT: Van de Vijver, Marc J.
12 ; APPLICANT: Bernards, Rene
13 ; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
14 ; FILE REFERENCE: 9301-188-999
15 ; CURRENT APPLICATION NUMBER: US/10/342,687
16 ; CURRENT FILING DATE: 2003-01-15
17 ; PRIOR APPLICATION NUMBER: 60/298,918

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Db 1628 TCTCTTTCAGAGTTGGGACACGCGGGGCTTCCTGATTCCTGGAATATAACTTTGTGTAAA 1687
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Db 1508 AAAATGGAATGCTTTTAAACAGCTTTTGGGGGTACTTGGAGTGTCTAATTAAGT 1567
QY 1560 GTCAAAATTTTGTAGTATGTTTGTGAGAGGCTCAACACAAACTGGAACATAGT 1619
Db 1568 GTCAAAATTTTGTAGTATGTTTGTGAGAGGTTCAACACAAACTGGAACATAGT 1627
QY 1620 TCTCTTCAAGTGTGGCAGACAGCGGGCTTCCGTGATCTGGAATTAACCTTTGTGAAA 1679

Db 2587 TTGAGATCTAAAGGCCCGCAGAGATCGTTTGATCCAAAGCCCTCTTATTTTTCAGAGGGGAAAA 2646
Qy 2640 TGGGGCCCTAGAGCTTACAGAGCATCTAGCTGTGGCTGGCACCCCTGGCCCTCACACAGA 2699
Db 2647 TGGGGCCCTAGAGCTTACAGAGCATCTAGCTGTGGCTGGCACCCCTGGCCCTCACACAGA 2706
Qy 2700 CTCGGAGTACGCTGGAGCTACAGGACACAGTCACTGAGGAGGCGCCCTGTTGCAATTCA 2759
Db 2707 CTCGGAGTACGCTGGAGCTACAGGACACAGTCACTGAGGAGGCGCCCTGTTGCAATTCA 2766
Qy 2760 CGGTGCGACCTCCACTTAACATCTTCAATAGTATGTCTTCTAGTCACTAAGTTAAA 2819
Db 2767 CGTTGCCACCTCCACTTAACATCTTCAATAGTATGTCTTCTAGTCACTAAGTTAAA 2826
Qy 2820 CTTTCCACCCAGAAAAGCACTTAGATATAATCTTAGAGTACTTTTCACTCTTCTAA 2879
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Qy 2880 GTCTCTTCCAGGCTCACTTTGAGTCTCTCTGGGGTTGATAGAAATTTCTCTGCTT 2939
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Qy 2940 CTGATAAGTCTTAATCTATCTATGTTAAATTTGACGATAGATTTCTGAGATA 2999
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Db 3007 AAATGTTCTGTTCACTT 3024

RESULT 2

US-10-823-155
; Sequence 155, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Heersche, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Monsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: NRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158

; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 155
; LENGTH: 3042
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-823-155

Query Match 99.0%; Score 2987.6; DB 14; Length 3042;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3012; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

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Db 8 GCTGGGGGCGACGGCGCGAGCTCGAGGGCGGGCGGGCGGGGAGAGGAGCGAC 67
Qy 61 CGGGCGGCTCGTAGCGGGGCGCGGATCCCGAGTGGCGGCGCGGAGCTCGAAAAAGAGA 120
Db 68 CGGGCGGCTCGTAGCGGGGCGCGGATCCCGAGTGGCGGCGCGGAGCTCGAAAAAGAGA 127
Qy 121 TTCTCAGGCGCTGATTTTGAATGATGGGCTTGGGAAAGCGGGGTCGACGATGAGTCCG 180
Db 128 TTCTCAGGCGCTGATTTTGAATGATGGGCTTGGGAAAGCGGGTGGCAFCATGAGTCCG 187
Qy 181 CGGGCGGCTCGTAGCGGGGCGCGGATCCCGAGTGGCGGCGCGGAGCTCGAAAAAGAGA 240
Db 188 CGGGCGGCTCGTAGCGGGGCGCGGATCCCGAGTGGCGGCGCGGAGCTCGAAAAAGAGA 247
Qy 241 TTTCGAGCTCCCGGAGCGTGGACCTCCAGACACGAGATCAATGGAGCTGGAAGCGAGGTC 300
Db 248 TTTCGAGCTCCCGGAGCGTGGACCTCCAGACACGAGATCAATGGAGCTGGAAGCGAGGTC 307
Qy 301 GCGGGGCGGCTCGAGAGAGAGGCGCGTGGAGCTGGAAGAGAAAGAGTCCAGGAGAGG 360
Db 308 GCGGGGCGGCTCGAGAGAGAGGCGCGTGGAGCTGGAAGAGAAAGAGTCCAGGAGAGG 367
Qy 361 TGGAGAGCGAGCGGAGAGCGTGGACAAATCCAGTCCAGCCACAACTCCAGCTGGAAGA 420
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Qy 481 AGAGGCTCATCCGAGTGTGCAAGACCGATTAAGAGCGCTGCAAGGAAATACGGGAGG 540
Db 488 AGAGGCTCATCCGAGTGTGCAAGACCGATTAAGAGCGCTGCAAGGAAATACGGGAGG 547
Qy 541 TGCAGCAGGATGCTCCAGTTTTCAGAGAACAGACCACTGAGAGGAGGTCTCTCT 600
Db 548 TGCAGCAGGATGCTCCAGTTTTCAGAGAACAGACCACTGAGAGGAGGTCTCTCT 607
Qy 601 ACAGCTGAGCGCATGATCAATCAGATGAGGAGGTGAGGACACGTGTGAGGAGCGAA 660
Db 608 ACAGCTGAGCGCATGATCAATCAGATGAGGAGGTGAGGAGACACGTGTGAGGAGCGAA 667
Qy 661 TAGAGAGGTCAACAAAAGGGGATGAGTGTAGCTTCCAGAGACCTGAGTGAARACA 720
Db 668 TAGAGAGGTCAACAAAAGGGGATGAGTGTAGCTTCCAGAGACCTGAGTGAARACA 727
Qy 721 ACAGCAGAGAGAGAGCTCCAGGCTCAGTGGAGCTCAGGCGGAGGCTGAGGAGGAG 780

Db 728 ACGACCAAGACAGAGCTCCAAAGCCCTCAGTGAAGCCTCAGGCCAGGCTGAGGCGACAG 787
Qy 781 GCGTCCACACACAGAGGTGCCAAAGGAAAGGAAACGCTGCTTGGTAAACAGCAAGTCCC 840
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Qy 841 AGACACCAAGCCCGAAGTTCGGAAGTGGTTTGGATTCAGAGAGCAAGTTGAGAAAGG 900
Db 848 AGACACCAAGCCCGAAGTTCGGAAGTGGTTTGGATTCAGAGAGCAAGTTGAGAAAGG 907
Qy 901 AANCCATGATCCAGAGTGGTGAATGAGAGCCTCAGAGGAGCAGGCTGCCGACAGAGC 960
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Db 1028 GAGAACTGGGCGAGACCCOACAGGTCGAGGCTGCCCTGTCACTGAGCCAGGAAATCCAG 1087
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Qy 1201 ATGAAAATGAGAGAGATCTGAGACAGACAGCAGCCCTGCCAGGGAATGACAGAA 1260
Db 1208 ATGAAAATGAGAGAGATCTGAGACAGACAGCAGCCCTGCCAGGGAATGACAGAA 1267
Qy 1261 ACATAGTGTCTTTTAAATGTTAGATCAGAAAAGAGACACATTAATTTACTTGATCAGC 1320
Db 1268 ACATAGTGTCTTTTAAATGTTAGATCAGAAAAGAGACACATTAATTTACTTGATCAGC 1327
Qy 1321 GTGAAAAGGGGAATCATACACTCTGAATTTGAACTGGAAATCAATATTTACACAGGGCC 1380
Db 1328 GTGAAAAGGGGAATCATACACTCTGAATTTGAACTGGAAATCAATATTTACACAGGGCC 1387
Qy 1381 GAAGAGATGACTTTAAATGTTCAAGGAGCTGAATCTGAAACTGTGAATGTACTA 1440
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Db 1688 TTAAACGCCACCTATAGAGAGTCCATCTGCTGTGAAGGAGACAGAGAACTCTGGTT 1747
Qy 1740 CCGTCTGCTGTCCAGTGTCTTAOCAGAGTGTGTGTGCCAGCCTGTACTGTCTCACT 1799
Db 1748 CCGTCTGCTGTCCAGTGTCTTAOCAGAGTGTGTGTGCCAGCCTGTACTGTCTCACT 1807
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Db 1808 GAAAAGCTGGCTTAATGCTCTGTGTAGTCACTCTGATTTGACAAATCAATCAAT 1867
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Qy 2040 TTTACTTTGCTTCTGTGTGGGCAAAAGCAACATCTTCCCTAAATATATATTACCAAGAA 2099
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Db 668 TAGAAGAGGTCAACAAAGGGGAATGAAAGCTGTAGCTTCAGAGACCTGAGTGAAGAACA 727
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Db 728 AGACACAGAGACAGAGCTCCAGAGCCCTCAGTGAAGCCTCAGCCACAGSCTGCAGGACGAG 787
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Db 1748 CCGTCTCTGTCTGACAGTGCCTGTACCAAGTCTGTGTGCGAGCCTGTACTGTCTCACT 1807
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Qy 1980 TCAATTTTAAATGACAAAAGCTATTTAAGTGGCTTAGAATTTGAACATTTGTGTCTTTA 2039
Db 1988 TCAATTTTAAATGACAAAAGCTATTTAAGTGGCTTAGAATTTGAACATTTGTGTCTTTA 2047
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Db 2168 CAGAGCATGGTGAAGGCGCAAGGCTATGAGAGGCGAAG--TTTGTGTGTGACAGAGATCTGTGCC 2226
Qy 2220 TACTTTTACTGGAGTAAAAAGAAAACAAAGTTCAATGATGTCGAAAGATATATACAGTG 2279
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Db 2347 ACATTTAGCTTGTGTAAATGACTCAAAAACCTGATTTTAAATCAAGTTAATGTGAAT 2406
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RESULT 4
US-10-210-120-114
; Sequence 114, Application US/10210120
; Publication No. US20030175736A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Rubin, Mark A.
; APPLICANT: Sreekumar, Arur.
; TITLE OF INVENTION: Expression Profile of Prostate Cancer
; FILE REFERENCE: UM-C7221
; CURRENT APPLICATION NUMBER: US/10/210,120
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/309,581
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/334,468
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 114
; LENGTH: 3042
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-210-120-114

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Db 2827 GTTTCACACCAAGGACAACTTAGATAAAATCTAGAGTACTTTCATCTCTCTAA 2886
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 Qy 3000 AAATGTTCTGTTCACTT 3017
 Db 3007 AAATGTTCTGTTCACTT 3024
 RESULT 5
 US-10-341-434-120
 ; Sequence 120, Application US/10341434
 ; Publication No. US20030215835A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Origene Technologies
 ; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
 ; FILE REFERENCE: 9U 204 205 R1
 ; CURRENT APPLICATION NUMBER: US/10/341,434
 ; CURRENT FILING DATE: 2003-07-18
 ; PRIOR APPLICATION NUMBER: US 60/346,164
 ; PRIOR FILING DATE: 2002-01-15
 ; PRIOR APPLICATION NUMBER: US 60/346,119
 ; PRIOR FILING DATE: 2002-01-15
 ; NUMBER OF SEQ. ID NOS: 238
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 120
 ; LENGTH: 3042
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (148)..(1350)
 ; OTHER INFORMATION:
 US-10-341-434-120

Query Match 99.0%; Score 2987.6; DB 15; Length 3042;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 3012; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
 Qy 1 GCTGGGCGCA CGGCGCGAGCCGCGGAGCTCGAGGCGCGCGCGCGGCGGAGAGGCGACC 60
 Db 8 GCTGGGCGCA CGGCGCGAGCCGCGGAGCTCGAGGCGCGCGCGCGGCGGAGAGGCGACC 67
 Qy 61 CGGCGCGGCTCGTAGCGGCGCGCGGATCCCGAGTGGCGCGCGGAGGCTCGAAGAGAGA 120
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Db 248 TTGGAGCTCCCGGAGGCTGGAGCTTCAGACACGCGATCATGAGCTGGAAGGCGAGGCTCC 307
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 Db 308 GCAGGCGGCTTCAGAGAGAGGCGCGTGGAGGCTGAAGAAAGACGAGTTCAGAGGAGAGC 367
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 Db 368 TGGAGAAAGCGGCGGAGAGGCTTGAACAAAATCCAGTCCAGGCCACAACTTCCAGCTGGAGA 427
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 Db 428 GCGTCAACAGCTGTACCAAGGCGGAGGCTTGGTGAATTAACATCAACACAGGCTG 487
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2004, 01:46:51 ; Search time 5104.23 Seconds
(without alignments)
17650.880 Million cell updates/sec

Title: US-10-030-269A-7
Perfect score: 3017
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: em_estmu:*
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7: em_estro:*
8: em_hcc:*
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18: em_gss_inv:*
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21: em_gss_fun:*
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26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 1032.6 | 34.2 | 1201 | 9 | AL565763 |
| 3 | 955.4 | 31.7 | 1201 | 13 | EX447229 EX447229 |
| 4 | 946 | 31.4 | 1201 | 9 | AL565250 |
| 5 | 942.8 | 31.2 | 1039 | 9 | AL525714 |
| 6 | 936.6 | 31.0 | 1079 | 12 | BM548257 |
| 7 | 932.2 | 30.9 | 1201 | 9 | AL535069 |
| 8 | 922.8 | 30.6 | 1560 | 9 | AL525765 |
| 9 | 917 | 30.4 | 1201 | 9 | AL548068 |
| 10 | 903 | 29.9 | 1063 | 13 | EX402100 |
| 11 | 886.2 | 29.4 | 1058 | 12 | BM554565 |
| 12 | 867 | 28.7 | 1201 | 13 | EX358371 |
| 13 | 865.4 | 28.7 | 1201 | 13 | EX447230 |
| 14 | 862.6 | 28.6 | 1201 | 9 | AL572881 |
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| 17 | 834 | 27.6 | 913 | 13 | BQ228135 |
| 18 | 826.2 | 27.4 | 935 | 13 | BQ39789 |
| 19 | 822.4 | 27.3 | 1206 | 29 | AY414700 |
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| 21 | 783 | 26.1 | 900 | 13 | EX349102 |
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Search completed: April 3, 2004, 16:37:37
Job time : 5116.43 secs

OM nucleic - nucleic search, using sw model

Run on: April 3, 2004, 00:09:01 ; Search time 9047.21 Seconds
(without alignments)
16863.481 Million cell updates/sec

Title: US-i0-C30-269A-9
Perfect score: 3520
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3470272 segs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

| GenEmbl:* | Result No. | Score | Query Match | Length | DB | ID | Description |
|--------------|---------------|--------|----------------|--------|----|----------|-------------|
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| 2: gb_htg:* | 2 | 3520 | 100.0 | 3520 | 6 | BD093298 | Any-old b |
| 3: gb_in:* | 3 | 3520 | 100.0 | 3520 | 6 | BD123657 | Secretary |
| 4: gb_om:* | 4 | 3520 | 100.0 | 3520 | 9 | AK075556 | Homo sapi |
| 5: gb_ov:* | 5 | 3513.6 | 99.8 | 5233 | 9 | AF152308 | Homo sapi |
| 6: gb_pat:* | 6 | 3150.8 | 89.5 | 5257 | 9 | AF152307 | Homo sapi |
| 7: gb_pa:* | 7 | 3135.8 | 89.1 | 5254 | 9 | AF152306 | Homo sapi |
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| 9: gb_pr:* | 9 | 3129.2 | 88.9 | 5218 | 9 | AF152313 | Homo sapi |
| 10: gb_ro:* | 10 | 3123 | 88.7 | 5260 | 9 | AF152305 | Homo sapi |
| 11: gb_sts:* | 11 | 3120.2 | 88.6 | 5221 | 9 | AF152315 | Homo sapi |
| 12: gb_sy:* | 12 | 3112.4 | 88.4 | 5260 | 9 | AF152314 | Homo sapi |
| 13: gb_un:* | 13 | 3111.8 | 88.4 | 5260 | 9 | AF152311 | Homo sapi |
| 14: gb_vi:* | 14 | 3110.8 | 88.4 | 4666 | 9 | BC036674 | Homo sapi |
| 15: en_ba:* | 15 | 3107.6 | 88.3 | 5263 | 9 | AF152316 | Homo sapi |
| 16: en_fun:* | 16 | 3101.2 | 88.1 | 5251 | 9 | AF152312 | Homo sapi |
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| 18: en_in:* | 18 | 3091.6 | 87.8 | 5260 | 9 | AF152317 | Homo sapi |
| 19: en_mu:* | 19 | 2326.6 | 66.1 | 5254 | 10 | AY013759 | Mus muscu |
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| 25: en_ro:* | 25 | 2307 | 65.5 | 5230 | 10 | AY013761 | Mus muscu |
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| 28: en_un:* | 28 | 2297.6 | 65.3 | 5242 | 10 | AY013757 | Mus muscu |
| 29: en_vi:* | 29 | 2296 | 65.2 | 5248 | 10 | AY013760 | Mus muscu |
| 30: en_wi:* | 30 | 2294.6 | 65.2 | 5242 | 10 | AY013764 | Mus muscu |
| 31: en_xi:* | 31 | 2294.6 | 65.2 | 5341 | 10 | AY013767 | Mus muscu |
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| 35: en_ab:* | 35 | 2168.2 | 61.6 | 5299 | 9 | AF152303 | Homo sapi |
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| 39: en_ah:* | 39 | 1952.8 | 55.5 | 147172 | 9 | AC005688 | Homo sapi |
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| 41: en_aj:* | 41 | 1951.2 | 55.4 | 150893 | 2 | AC044871 | Homo sapi |
| 42: en_ak:* | 42 | 1951.2 | 55.4 | 184662 | 9 | AC025436 | Homo sapi |
| 43: en_al:* | 43 | 1692.8 | 48.1 | 10521 | 10 | AB114630 | Mus muscu |
| 44: en_am:* | 44 | 1662.6 | 47.2 | 3856 | 9 | HSBJ7609 | Homo sapi |
| 45: en_an:* | 45 | 1651.4 | 46.9 | 6230 | 6 | AX576261 | Sequence |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1
AX136409
LOCUS
DEFINITION
Sequence 331 from Patent EP:067182.
ACCESSION
AX136409
VERSION
AX136409.1 GI:14272813
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Ota, T., Isegai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and
Hayashi, K.
Secretory protein or membrane protein
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Helix Research Institute (JP)
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WLSYELQPAAVGAIHPFHVGLYTGELSTIRLDEADAPRHLVILVDRHGEPAUTSTA
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Query Match 100.0%; Score 3520; DS 6; Length 3520;
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1201 TTGTACACTGGCTGGTGTGCTCAGCGCGGCCCAACGCTGAGCGCGTGCAGCGCGGCGCAAG 1260
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| 3001 | ATCTATTACTAAADAATAATGATCTCTCTTTCTCTCTCTCTCTCTCTCTTTCTAAGAAACA | 3060 |
| 3061 | TTATGTGCACTTTGATACACAACTTCTTAACCAACTATATATACAGACCCAAAATTG | 3120 |
| 3061 | TTATGTGCACTTTGATACACAACTTCTTAACCAACTATATATACAGACCCAAAATTG | 3120 |
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| 3181 | TGTCITGTGTGTAGCCTACACCTTCTCTTGGTTTGGTTTCTTTCTTATACACTC | 3240 |
| 3181 | TGTCITGTGTGTAGCCTACACCTTCTCTTGGTTTGGTTTCTTTCTTATACACTC | 3240 |
| 3241 | TGAATGCTAATCTACTACTACACCTATGATGTTACTGAATCACTCCCATATGATG | 3300 |
| 3241 | TGAATGCTAATCTACTACTACACCTATGATGTTACTGAATCACTCCCATATGATG | 3300 |
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| 3361 | AATGCAACTATTACTTAGATGAACTTTAAGCTTTATGTTGAAATGAAATTCATATAT | 3420 |
| 3361 | AATGCAACTATTACTTAGATGAACTTTAAGCTTTATGTTGAAATGAAATTCATATAT | 3420 |
| 3421 | TTCTTTTGTACCTGTGAAAAGTGGAGTAGTGTTTTTTAAACCATTGTAATCAGCT | 3480 |
| 3421 | TTCTTTTGTACCTGTGAAAAGTGGAGTAGTGTTTTTTAAACCATTGTAATCAGCT | 3480 |
| 3481 | TTTGTGTATGAAGAACAAGTAAAAATTTCTTTCTTAATTC | 3520 |
| 3481 | TTTGTGTATGAAGAACAAGTAAAAATTTCTTTCTTAATTC | 3520 |

| | | | |
|-----------------|---|---------|------------|
| RESULT 2 | | | |
| BD093298 | | | |
| LOCUS | BD093298 | 3520 bp | DNA linear |
| DEFINITION | Amyloid beta alication regulatory factor. | | |
| PAT 27-AUG-2002 | | | |

ACCESSION BD093298
VERSION BD093298.1 GI:22638886
KEYWORDS WO 0104299-N/5.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3520)

| | |
|---|---|
| <p>AUTHORS</p> <p>Arakawa, H. and Morita, M.</p> <p>Ota, T., Isegaki, T., Nishikawa, I., Kawa, I., Yamazaki, M., Sato, S.,</p> | <p>TITLE</p> <p>Amlyoid beta aglilation regulatory factor</p> <p>JOURNAL</p> <p>Patent: WO 0104299-A 5 18-JAN-2001;</p> <p>URL: http://www.patentview.us/patent/qw/takao</p> |
|---|---|

COMMENT
OS Homo sapiens (human)
PN WO C104299-N/5
YURI KAWAI, MAYAHO YAMAZAKI, SUSUMU SATO, HIROYUKI ARAKAWA, MASASHIKO MORITA
HELIX RESERACH ANALYZED; KOGUCHI CH. ANALYZED; ADOOR, J. ANALYZED; KAWA

PD 18-JAN-2001
PF 06-JUL-2000 WO 2000JP04515
PR 08-JUL-1999 JP 99P 194179,18-OCT-1999 US 60/159386 PI
TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, YURI KAWAI, MAYAKO PI

YAMAZAKI,
PI SUSUMU SATO, HIROYUKI ARAKAWA, MASAHITO MORITA
PC C12N15/12, C07K16/18, C12N5/10, A61K45/00, A61K48/00, EC

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A61K31/711,
PC A61P25/28,G01N33/15,G01N33/50
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F2 Location/Qualifiers
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/db xref="taxon:9606"
FEATURES
source

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ORIGIN

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|-----------------------|---------|--------------|-------|--------------|
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| Best Local Similarity | 100.0%; | Pred. No. 0; | | |

Matches 352/; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
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| D6 | 1 | GGATTCAGGTTAACGCATGATTAAGAGGATTCGCTCATGGGAGGTCACAGCAGTGGTC | 80 |
| QY | 61 | CTGGTGGAAATTCGGAGGTGAATGACAAATGTCCCTGAAGTAATGGTTACTCACTGTGCG | 120 |
| QY | 61 | CTGGGGAATTCGGAGGTGAATGACAAATGTCCCTGAAGTAATGGTTACTCACTGTGCG | 120 |

[illegible]

| Accession | Sequence | Length |
|-----------|--|--------|
| QY | CGTGACTCTGGAGCCAAATGGACAGGTCATCTGCTCACTGACACCTCATGTTCCCTCAAG | 240 |
| DB | CGTGACTCTGGAGCCAAATGGACAGGTCATCTGCTCACTGACACCTCATGTTCCCTCAAG | 240 |

Q7 241 CTGGTGCACCTACAGAAATTACTACTGTTGGTGCTGACAGCGCCCTGTGGATCCGGAG 300
|||||
|||||

D6 241 CTGGTGCACCTACAGAAATTACTACTGTTGGTGCTGACAGCGCCCTGTGGATCCGGAG 300
|||||
|||||

| | | | |
|----|-----|---|-----|
| QY | 301 | AGCGTCTCGGCGCTATGAGCTGTTGTTGACTCGCGGGGATGGGGGCTCGCCTTCGCTGTGG | 360 |
| | | | |
| Db | 301 | AGCGTCTCGGCGCTATGAGCTGTTGTTGACTCGCGGGGATGGGGGCTCGCCTTCGCTGTGG | 360 |

[illegible][illegible]

| | | |
|----|--|--|
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| | | 491 GTGTCCGGCATGGGACCGCGCGAGAAAGCGCGCTGTTCTTACTTCGCTGGTGAG 540 |
| Db | | 481 GTGTCCGGCATGGGACCGCGCGAGAAAGCGCGCTGTTCTTACTTCGCTGGTGAG 540 |

541 CGCGGGTGGCGAGCA CGCACTGT CGAGCTACGTTGCGTGCACGCGAGAGCGGCAAG 600
QY

541 CGCGGGTGGCGAGCA CGCACTGT CGAGCTACGTTGCGTGCACGCGAGAGCGGCAAG 600
Db

[illegible]

661 GGGGGGAGACGGGGCGTGGCGCTCTGGGAGACAGTGGAGCTGCAGGTGTGGTCTG 720

| | | | | | | | |
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| QY | 721 | GACGAGAACGACAACGGCGCGGCACTGCTGGCGACTCCGGCTGGCAGCGCAGGAGGGCA | 780 | DB | 1621 | AGCTGGACGCTTTAAATAGCGACCGCGCAACCCCAACATCGGCTCCGGTGA GTGGCC | 1680 |
| QY | 721 | GACGAGAACGACAACGGCGCGGCACTGCTGGCGACTCCGGCTGGCAGCGCAGGAGGGCA | 780 | DB | 1681 | GACAAATTCATTATCCAGAGTCTCTGCAATCATCTCCATCCGGCAGGAGGCTACTAAC | 1740 |
| DB | 721 | GACGAGAACGACAACGGCGCGGCACTGCTGGCGACTCCGGCTGGCAGCGCAGGAGGGCA | 780 | DB | 1681 | GACAAATTCATTATCCAGAGTCTCTGCAATCATCTCCATCCGGCAGGAGGCTACTAAC | 1740 |
| QY | 781 | GTTAGCGAGTTGTTACCGCGGTGGTGGGTGGCGGCGACGCTGGTGGCGAAAGTGGCGGG | 840 | QY | 1741 | AGCCAAATTCACAAAGTGACTTCATACCTTCGGGMAAAGAGAGAGACCAAGAAAAG | 1800 |
| DB | 781 | GTTAGCGAGTTGTTACCGCGGTGGTGGGTGGCGGCGACGCTGGTGGCGAAAGTGGCGGG | 840 | DB | 1741 | AGCCAAATTCACAAAGTGACTTCATACCTTCGGGMAAAGAGAGAGACCAAGAAAAG | 1800 |
| QY | 841 | GTGAGCGCTGACTCCGGCTATACCGCTTGGCTGGCTGCTTACAGATTGCACCGGGCGGTC | 900 | QY | 1801 | ARGMAAAGAGAAAGGTAACAGACCCAGGAGAAAAAGAAAGAAAGCAACAGCACT | 1860 |
| DB | 841 | GTGAGCGCTGACTCCGGCTATACCGCTTGGCTGGCTGCTTACAGATTGCACCGGGCGGTC | 900 | DB | 1801 | ARGMAAAGAGAAAGGTAACAGACCCAGGAGAAAAAGAAAGAAAGCAACAGCACT | 1860 |
| QY | 901 | GGCGGCACATCCGGCTTCACGCTGGGGCTGTACACTGGCGAGATCAGCAACGACGCATC | 960 | QY | 1861 | GACACAGTGAACACGAGTGAGTCTCTCAATGGAAACAGGCACCTTAGCCAGTTTGTAAAT | 1920 |
| DB | 901 | GGCGGCACATCCGGCTTCACGCTGGGGCTGTACACTGGCGAGATCAGCAACGACGCATC | 960 | DB | 1861 | GACACAGTGAACACGAGTGAGTCTCTCAATGGAAACAGGCACCTTAGCCAGTTTGTAAAT | 1920 |
| QY | 961 | CTGGATGAGGGCGAGGCTTCGGCGCCACCGGCTCGTGGTGGTGGTGAAGGACCAAGTGAG | 1020 | QY | 1921 | ANTGGCAATCTCTCCATGTACGATTCGCTGCTCTTTTCCTATCTACATGAGGCGCT | 1980 |
| DB | 961 | CTGGATGAGGGCGAGGCTTCGGCGCCACCGGCTCGTGGTGGTGGTGAAGGACCAAGTGAG | 1020 | DB | 1921 | ANTGGCAATCTCTCCATGTACGATTCGCTGCTCTTTTCCTATCTACATGAGGCGCT | 1980 |
| QY | 1021 | CCCGGGCTGACGTCCAGGGCCAGTGCGCTGGTGGTGGTGGTGGAGAAAGGGCGCCCA | 1080 | QY | 1981 | CTTAGAGACCTCAGAAATCTGCGAGAAAGTTCCTGCTGCTGTAGAAACGATTTAAGAG | 2040 |
| DB | 1021 | CCCGGGCTGACGTCCAGGGCCAGTGCGCTGGTGGTGGTGGTGGAGAAAGGGCGCCCA | 1080 | DB | 1981 | CTTAGAGACCTCAGAAATCTGCGAGAAAGTTCCTGCTGCTGTAGAAACGATTTAAGAG | 2040 |
| QY | 1081 | AAGAGCTGTGGGGGCTCAGTGCGGGCTGTGGATCCCGAAGCGGCTCTGGTGGATATT | 1140 | QY | 2041 | GTTTTCTGATAAGGCTTTACTAAGTCTGCTGTTAACTCTTTCTCTCCACTCTGGCTGT | 2100 |
| DB | 1081 | AAGAGCTGTGGGGGCTCAGTGCGGGCTGTGGATCCCGAAGCGGCTCTGGTGGATATT | 1140 | DB | 2041 | GTTTTCTGATAAGGCTTTACTAAGTCTGCTGTTAACTCTTTCTCTCCACTCTGGCTGT | 2100 |
| QY | 1141 | AACGTGTACCTCATCATCGGACATCTGTGGGGTTCACGGCTGTGGTGTCAAGCTGTGT | 1200 | QY | 2101 | TTTCAGACCTTAAAGAGCAGCCAGTTTCCTTCTCTCCGCGCGAAGAGAGAGGCTT | 2160 |
| DB | 1141 | AACGTGTACCTCATCATCGGACATCTGTGGGGTTCACGGCTGTGGTGTCAAGCTGTGT | 1200 | DB | 2101 | TTTCAGACCTTAAAGAGCAGCCAGTTTCCTTCTCTCCGCGCGAAGAGAGAGGCTT | 2160 |
| QY | 1201 | TTGTACACTGGGCTGGTGTCTCAGGGCGGCCACCGGTGAGCGGTGGCGCGCGGCAAG | 1260 | QY | 2161 | CCGACCGCGCGAGTGAAGGTTGACTCTCTGCGCTGTGCTCCGGGAGTCTCTTTGA | 2220 |
| DB | 1201 | TTGTACACTGGGCTGGTGTCTCAGGGCGGCCACCGGTGAGCGGTGGCGCGCGGCAAG | 1260 | DB | 2161 | CCGACCGCGCGAGTGAAGGTTGACTCTCTGCGCTGTGCTCCGGGAGTCTCTTTGA | 2220 |
| QY | 1261 | CCGACGCTGGTGTCTCAGGGCGGTGGGAGTTGGTCTTACTCCGACAGAGAGGCGAG | 1320 | QY | 2221 | TGACACTTCGAGGGCAGGCTGAAAGTTTGTAGATTGAGCAGCTTGGAGGTTTGGGCA | 2280 |
| DB | 1261 | CCGACGCTGGTGTCTCAGGGCGGTGGGAGTTGGTCTTACTCCGACAGAGAGGCGAG | 1320 | DB | 2221 | TGACACTTCGAGGGCAGGCTGAAAGTTTGTAGATTGAGCAGCTTGGAGGTTTGGGCA | 2280 |
| QY | 1321 | AGGGTGTGCTCTCAGAGAGCGCGCCGAAGACGACCTCATGGGCTTCAGGCCAAGCCTT | 1380 | QY | 2281 | CTGGGTATGTACCTAACCGCGGGTATGGAGTGGCAGATTTGGCTGAGACGAGCGAC | 2340 |
| DB | 1321 | AGGGTGTGCTCTCAGAGAGCGCGCCGAAGACGACCTCATGGGCTTCAGGCCAAGCCTT | 1380 | DB | 2281 | CTGGGTATGTACCTAACCGCGGGTATGGAGTGGCAGATTTGGCTGAGACGAGCGAC | 2340 |
| QY | 1381 | CAGCTGTCTCGAGAGATTGTTTAAATCCTCCAGTGAACACAGAGACCGCAACCCCTGAC | 1440 | QY | 2341 | TTAGACTTAATTTGTTCAAGGAGGCAAGAAACAAAGACAAATTAACGCGGAGATTTC | 2400 |
| DB | 1381 | CAGCTGTCTCGAGAGATTGTTTAAATCCTCCAGTGAACACAGAGACCGCAACCCCTGAC | 1440 | DB | 2341 | TTAGACTTAATTTGTTCAAGGAGGCAAGAAACAAAGACAAATTAACGCGGAGATTTC | 2400 |
| QY | 1441 | TGGGTTTACTCTGCTTCCCTGAGAGCAGGCTGCACAGCTCTGTGCACCTTAGAGAGGCT | 1500 | QY | 2401 | AGTATGGAGGGGAAGTGTAAACTTAAAGGGAACAGACCTTCTAAATCTTACACTCAGA | 2460 |
| DB | 1441 | TGGGTTTACTCTGCTTCCCTGAGAGCAGGCTGCACAGCTCTGTGCACCTTAGAGAGGCT | 1500 | DB | 2401 | AGTATGGAGGGGAAGTGTAAACTTAAAGGGAACAGACCTTCTAAATCTTACACTCAGA | 2460 |
| QY | 1501 | GGCATTTACGGGCTGGTCCAGGAGGGGCTGATCAGCAGTGGCCACAGTATCCAGTGCA | 1560 | QY | 2461 | GSTGGCAGCGCCCTCTAGGAGACAAACTACCCACTGACAAAGCTTTAGGAGACCT | 2520 |
| DB | 1501 | GGCATTTACGGGCTGGTCCAGGAGGGGCTGATCAGCAGTGGCCACAGTATCCAGTGCA | 1560 | DB | 2461 | GSTGGCAGCGCCCTCTAGGAGACAAACTACCCACTGACAAAGCTTTAGGAGACCT | 2520 |
| QY | 1561 | ACACAGAACACAGAGGAGAGAGTGTCCCTCAGCTGGTGGGGTGTCAACAGCAAC | 1620 | QY | 2521 | AAAGTCTGTTGGCTGTGAGCTCATTAACCTAAAACTGTGATCATACCTGCAAGCCACA | 2580 |
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| QY | 1621 | AGCTGGACTTTAAATACGAGACCGGCAACCCCAACATCCGGTTCGGGTGAGTGGCC | 1680 | QY | 2581 | GTTCAAGTGTTTAAACAGAGAACCCCTGGGMAAAGAGAGAGACTGAGTGTTCCTTA | 2640 |

| | | |
|------|---|------|
| 721 | GACGAGAACGACACACGCGCGGGACATGCTGGCGACTCCGGCTGGCAGCGCAGAGAGGCGCA | 780 |
| 721 | GACGAGAGCAGACACGCGCGCGGACATGCTGGCGACTCCGGCTGGCAGCGCAGAGAGGCGCA | 780 |
| 761 | GTTTAGCGAGTTGGTACCGCGGGTCCGTTGGGTGGCGGCACAGTGGTGGCGAAAGTGGCGCGCG | 840 |
| 761 | GTTTAGCGAGTTGGTACCGCGGGTCCGTTGGGTGGCGGCACAGTGGTGGCGAAAGTGGCGCGCG | 840 |
| 841 | GTGAGCGCTGACTCCGGCTATACCGCTATACCGCTTGGCTGTCTTACGAGTTGCACCGCGCGCGGTC | 900 |
| 841 | GTGAGCGCTGACTCCGGCTATACCGCTATACCGCTTGGCTGTCTTACGAGTTGCACCGCGCGCGGTC | 900 |
| 901 | GGCGSCACACATCCGTTCCACGTGGGGCTGTACACTGGCGAGATACGACGACACGCAATC | 960 |
| 901 | GGCGSCACACATCCGTTCCACGTGGGGCTGTACACTGGCGAGATACGACGACACGCAATC | 960 |
| 961 | CTGAGTAGGCGCGACGCTCCGCGCCACACCGCTGCTGGTGGTGGTGAAGGACCACGGTGAG | 1020 |
| 961 | CTGAGTAGGCGCGACGCTCCGCGCCACACCGCTGCTGGTGGTGGTGAAGGACCACGGTGAG | 1020 |
| 1021 | CCGCGGCTGACGTCCAGCGGCAAGGTGCTGGTGGCTGGTGGAGAACGCGCCACCGCCCA | 1080 |
| 1021 | CCGCGGCTGACGTCCAGCGGCAAGGTGCTGGTGGCTGGTGGAGAACGCGCCACCGCCCA | 1080 |
| 1081 | AAGACGTCGTGGCGGGCTCAGTGGCGGCTGTGGATCCCGAAGCGGCTCTGGTGGATATT | 1140 |
| 1081 | AAGACGTCGTGGCGGGCTCAGTGGCGGCTGTGGATCCCGAAGCGGCTCTGGTGGATATT | 1140 |
| 1141 | AACGCTGTAACCTCATCAGCGGCAATCTGTGGGAGTGCAGGCTGCTGGTGTCTACGCTGCTG | 1200 |
| 1141 | AACGCTGTAACCTCATCAGCGGCAATCTGTGGGAGTGCAGGCTGCTGGTGTCTACGCTGCTG | 1200 |
| 1201 | TTGTACACTGGGCTGGTGTCTCAGCGCGCCCAACCGTGGAGCGGCTGGCGGCGCGGCAAG | 1260 |
| 1201 | TTGTACACTGGGCTGGTGTCTCAGCGCGCCCAACCGTGGAGCGGCTGGCGGCGCGGCAAG | 1260 |
| 1261 | CCACGCTGGTGTGCTCCAGCGCGCTGGGAGTTGGTCTTACTCCGACGACGAGAGGCGAG | 1320 |
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| 1321 | AGGGTGTGCTGTCCAGAGAGCGCGCCCAAGACGGAGCTCATGGCTTACGCGCCACAGCCTT | 1380 |
| 1321 | AGGGTGTGCTGTCCAGAGAGCGCGCCCAAGACGGAGCTCATGGCTTACGCGCCACAGCCTT | 1380 |
| 1381 | CAGCTGTCTCGAGAGATTGTTTAAATCTCTCCAGTGAACACGACGACGCCAACCTGCAC | 1440 |
| 1381 | CAGCTGTCTCGAGAGATTGTTTAAATCTCTCCAGTGAACACGACGACGCCAACCTGCAC | 1440 |
| 1441 | TGGCGTTACTCTGCCTCCCTGAGACGAGCATGCAACAGCTCTGTCCACCTTAGAGAGGCT | 1500 |
| 1441 | TGGCGTTACTCTGCCTCCCTGAGACGAGCATGCAACAGCTCTGTCCACCTTAGAGAGGCT | 1500 |
| 1501 | GGGATTTACGGGCTGGTCCAGAGGGGCTGATCAGCAGTGGCGAACAGTATCCAGTCA | 1560 |
| 1501 | GGGATTTACGGGCTGGTCCAGAGGGGCTGATCAGCAGTGGCGAACAGTATCCAGTCA | 1560 |
| 1561 | ACACAGAACACGACGACGAGAGAGTGTCCCTCCAGTCCGGTGGCGGTCTCAACAGCAAC | 1620 |
| 1561 | ACACAGAACACGACGACGAGAGAGTGTCCCTCCAGTCCGGTGGCGGTCTCAACAGCAAC | 1620 |
| 1621 | AGCTGGAAGCTTTAAATACGACACGAGCAACCCCAACCAATCCGGTCCGGTGGATTGCC | 1680 |

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|-----------------------|---|--|-----------|--------------|-----------------|
| LOCUS | BD123657 | 3520 bp | DNA | linear | PAT 18-SEP-2002 |
| DEFINITION | Secretory protein or membrane protein. | | | | |
| ACCESSION | BD123657 | | | | |
| VERSION | BD123657.1 | GI-23218602 | | | |
| KEYWORDS | JP 2002017376-A/166. | | | | |
| KEYWORDS | Hom sapiens (human) | | | | |
| ORGANISM | Hom sapiens | | | | |
| ORGANISM | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| ORGANISM | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | |
| REFERENCE | 1 (bases 1 to 3520) | | | | |
| AUTHORS | Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K. | | | | |
| TITLE | Secretory protein or membrane protein | | | | |
| JOURNAL | Patent: JP 2002017376-A 166 22-JAN-2002; | | | | |
| JOURNAL | HELIX RESEARCH INSTITUTE | | | | |
| COMMENT | OS Homo sapiens (human) | | | | |
| COMMENT | PN JP 2002017376-A/166 | | | | |
| COMMENT | PD 22-JAN-2002 | | | | |
| COMMENT | PF 07-JUL-2000 JP 2000253173 | | | | |
| COMMENT | PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, YURI KAWAI, TOMOYASU SUGIYAMA, | | | | |
| COMMENT | PI SUGIYAMA, | | | | |
| COMMENT | PI KOJI HAYASHI | | | | |
| COMMENT | PC | | | | |
| COMMENT | C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10, | | | | |
| COMMENT | 10, | | | | |
| COMMENT | PC C12P21/02,C12Q1/68//C12P21/09,C12N15/00,C12N5/00 OC | | | | |
| FEATURES | Secretory protein or membrane protein | | | | |
| source | PH Key Location/Qualifiers | | | | |
| source | FT CDS (40)..(1875). | | | | |
| source | Location/Qualifiers | | | | |
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| source | /mol_type="genomic DNA" | | | | |
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| ORIGIN | | | | | |
| Query Match | 100.0%; | Score 3520; | DB 6; | Length 3520; | |
| Best Local Similarity | 100.0%; | Pred. No. 0; | | | |
| Matches 3520; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; | |
| Qy | 1 | GAATTGAGTTTACGGCATTTGATTAAGGGATTCCTTCATGGCAGTCAAGCATGGTTC | 60 | | |
| Db | 1 | GAATTCAGGTTACGGCATTTGATTAAGGGATTCCTTCATGGCAGTCAAGCATGGTTC | 60 | | |
| Qy | 61 | CTGGTGGAAATTCGTGAGCGTGAATGACAATGTCCCTGAGCTAATGCTTACTTCACTGTG | 120 | | |
| Db | 61 | CTGGTGGAAATTCGTGAGCGTGAATGACAATGTCCCTGAGCTAATGCTTACTTCACTGTG | 120 | | |
| Qy | 121 | CTCCCTGTGCAGAGGATGCTCAGGTGGGTACGGTTCATTCGCTCATGATACGGTGTGGAT | 180 | | |
| Db | 121 | CTCCCTGTGCAGAGGATGCTCAGGTGGGTACGGTTCATTCGCTCATGATACGGTGTGGAT | 180 | | |
| Qy | 181 | CGTGAATCTGGAGCATGGCAGTGTATCTGCTCACTGACACCTCATGTTCCCTTCAAG | 240 | | |
| Db | 181 | CGTGAATCTGGAGCATGGCAGTGTATCTGCTCACTGACACCTCATGTTCCCTTCAAG | 240 | | |
| Qy | 241 | CTGGTGTCACTACAGAAATTAATCTACTCTGTTGGTGGTGGACAGCGCCCTGGACCGGAG | 300 | | |
| Db | 241 | CTGGTGTCACTACAGAAATTAATCTACTCTGTTGGTGGTGGACAGCGCCCTGGACCGGAG | 300 | | |

| | | | |
|----|------|---|------|
| Db | 3121 | AGGAAATAATGTTTTCTATACAGTGAAGGATTTTCAATCACTATATCTGTGACT | 3180 |
| Qy | 3181 | TGTCCTGGTGCTAGCCTACACCTTCCTCTGGGTTAGTTTCCTTTCTATAACACTC | 3240 |
| Db | 3181 | TGTCCTGGTGCTAGCCTACACCTTCCTCTGGTGGTTTCCTTTCTATAACACTC | 3240 |
| Qy | 3241 | TGAATGCTAATCTACTACACCTATGATGATTAAGTGAATCAATCTCCCATATGATG | 3300 |
| Db | 3241 | TGAATGCTAATCTACTACACCTATGATGATTAAGTGAATCAATCTCCCATATGATG | 3300 |
| Qy | 3301 | CTGATGCTATGCTAAGACTCCTGAAATATATCTACTCTGCTTGTGTATGTGAATGTT | 3360 |
| Db | 3301 | CTGATGCTATGCTAAGACTCCTGAAATATATCTACTCTGCTTGTGTATGTGAATGTT | 3360 |
| Qy | 3361 | AATGCAACTATTAAGTAGGTGAACCTTTAGCTTTATTGTTGAATGTAATCCATATAT | 3420 |
| Db | 3361 | AATGCAACTATTAAGTAGGTGAACCTTTAGCTTTATTGTTGAATGTAATCCATATAT | 3420 |
| Qy | 3421 | TTCTTTTGTACCTGTGAAAAGTGAAGTAGTGTTTTTTAAACCATGTTTAATCAGCT | 3480 |
| Db | 3421 | TTCTTTTGTACCTGTGAAAAGTGAAGTAGTGTTTTTTAAACCATGTTTAATCAGCT | 3480 |
| Qy | 3481 | TTTGTGTATGAAGACACAGATAAAATTTCTTTCTTAAATC | 3520 |
| Db | 3481 | TTTGTGTATGAAGACACAGATAAAATTTCTTTCTTAAATC | 3520 |

RESULT 4
 AK075556
 LOCUS
 DEFINITION
 to Homo. sapiens cDNA PSEC0256 fig, c-one N12RP3300549, highly similar
 to Homo. sapiens protocadherin alpha 12 (PCDH-alpha12) mRNA.

| | |
|------------|--|
| RESULT 4 | |
| AK075556 | |
| LOCUS | AK075556 3520 bp mRNA linear PRI 03-SEP-2002 |
| DEFINITION | Homo sapiens cDNA PSEC0256 f1s, c-one N2R23003549, highly similar to Homo sapiens protocadherin alpha 12 (PCDH-alpha12) mRNA. |
| ACCESSION | AK075556 |
| VERSION | AK075556.1 GI:22761781 |
| KEYWORDS | oligo capping; f1s (full insert sequence). |
| SOURCE | Homo sapiens (human) |
| ORGANISM | Homo sapiens |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |
| AUTHORS | 1 Ota, T., Nishikawa, T., Suzuki, Y., Kawai-Hio, Y., Hayashi, K., Ishii, S., Saito, K., Yamamoto, J., Wakamatsu, A., Nagai, T., Nakamura, Y., Nagahari, K., Sugano, S. and Isogai, T. |
| TITLE | HRI human cDNA sequencing project |
| JOURNAL | Unpublished |
| REFERENCE | 2 (bases 1 to 3520) |
| AUTHORS | Isogai, T. and Yamamoto, J. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1332-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) |
| COMMENT | HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass sequencing, clone selection and full insert sequencing: Helix Research Institute (supported by Japan Key Technology Center etc.); cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center. |
| FEATURES | Location/Qualifiers |
| source | 1. 3520 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /cnaes="N2R23003549" |

/cell_line="NT2"
/cell_type="teratocarcinoma"
/clone_lib="NT2RP3"
/note="cloning vector: pME18SFL3-mRNA from NT2 neuronal
precursor cells after 2-weeks retinoic acid (RA)
induction"

ORIGIN

Query Match 100.0%; Score 3520; DB 9; Length 3520;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3520; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
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| Qy | 1 | GAATACAGTTAAGCCATGATTAAGGGAATTCCTTCATGGCAGGTACAGCATGGTC | 63 |
| Ds | 1 | GAATTCAGGTTAAGCCATGATTAAGGGAATTCCTTCATGGCAGGTACAGCATGGTC | 60 |
| Qy | 61 | CTGGTGGAAATCTCGACGTGAATGACATGTCCCTGAAGTAAAGGTTACTTCACTGTG | 120 |
| Ds | 61 | CTGGTGGAAATCTCGACGTGAATGACATGTCCCTGAAGTAAAGGTTACTTCACTGTG | 120 |
| Qy | 121 | CTCCCTGTGCAAGAGGATGCTCAGGTGGGTACCGTCAATGGCCCTGATTAGCGTGTG | 180 |
| Ds | 121 | CTCCCTGTGCAAGAGGATGCTCAGGTGGGTACCGTCAATGGCCCTGATTAGCGTGTG | 180 |
| Qy | 181 | CGTGACTCTGGAGCCATGGACAGGTTCATCTGCTCAGTACACCTCATGTTCCCTCAAG | 240 |
| Ds | 181 | CGTGACTCTGGAGCCATGGACAGGTTCATCTGCTCAGTACACCTCATGTTCCCTCAAG | 240 |
| Qy | 241 | CTGGTGTCCACCTACAAAGATTAATCTACTGCTGGTGGTGGACAGCGCCCTGGAC | 300 |
| Ds | 241 | CTGGTGTCCACCTACAAAGATTAATCTACTGCTGGTGGTGGACAGCGCCCTGGAC | 300 |
| Qy | 301 | AGCGGTCTGGGCTATGAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG | 360 |
| Ds | 301 | AGCGGTCTGGGCTATGAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG | 360 |
| Qy | 361 | GCACGGCTAGAGTGTCCCTGGAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG | 420 |
| Ds | 361 | GCACGGCTAGAGTGTCCCTGGAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG | 420 |
| Qy | 421 | CAGCCGAGTACACAGTGTTCGTGAAGAGAGAACACCGCGGGGCTGCCACATCTTACG | 480 |
| Ds | 421 | CAGCCGAGTACACAGTGTTCGTGAAGAGAGAACACCGCGGGGCTGCCACATCTTACG | 480 |
| Qy | 481 | GTCTCGGCATGGACGGAGCGCGAGAGAAAGGCGCTGGTGTCTACTCGCTGGTGGAG | 540 |
| Ds | 481 | GTCTCGGCATGGACGGAGCGCGAGAGAAAGGCGCTGGTGTCTACTCGCTGGTGGAG | 540 |
| Qy | 541 | CGCGGGTGGCGGAGCACCGCACTGTCTGAGCTAGCTGTGGTGTCTGAGTGGAGAG | 600 |
| Ds | 541 | CGCGGGTGGCGGAGCACCGCACTGTCTGAGCTAGCTGTGGTGTCTGAGTGGAGAG | 600 |
| Qy | 601 | GTGTACGGCTGTGAGCGGCTAGACACAGAGAGCTGGAGCTGCTGCAATTCAGGTGAGC | 660 |
| Ds | 601 | GTGTACGGCTGTGAGCGGCTAGACACAGAGAGCTGGAGCTGCTGCAATTCAGGTGAGC | 660 |
| Qy | 661 | GGCGCGAGCGCGCGGTGGCGGCTCTGGGAGCAACAGTGTGAGCTGTGAGTGTGGTGG | 720 |
| Ds | 661 | GGCGCGAGCGCGCGGTGGCGGCTCTGGGAGCAACAGTGTGAGCTGTGAGTGTGGTGG | 720 |
| Qy | 721 | GACGAGACGACACAGCGCGGCACTGCTGGGAGCTCCGGTGGCAGCGAGAGGCGCA | 780 |
| Ds | 721 | GACGAGACGACACAGCGCGGCACTGCTGGGAGCTCCGGTGGCAGCGAGAGGCGCA | 780 |

| | | | |
|----|------|---|------|
| Qy | 781 | GTTAGCGAGTGTGTACCGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG | 840 |
| Ds | 781 | GTTAGCGAGTGTGTACCGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG | 840 |
| Qy | 841 | GTGAGCGCTGACTCCGGCTATAACGCTTGCGTGTCTCTACGAGTTGCAACCGCGGGT | 900 |
| Ds | 841 | GTGAGCGCTGACTCCGGCTATAACGCTTGCGTGTCTCTACGAGTTGCAACCGCGGGT | 900 |
| Qy | 901 | GGCGCGCAATCCCGTCCACGTTGGGCTGTACATCTGGCGAGATGACACGACGATC | 960 |
| Ds | 901 | GGCGCGCAATCCCGTCCACGTTGGGCTGTACATCTGGCGAGATGACACGACGATC | 960 |
| Qy | 961 | CTGGATGAGCGGAGCGCTCCGCGCACCGCTGTGGTGTGGTGTGGTGTGGTGTGGTGT | 1020 |
| Ds | 961 | CTGGATGAGCGGAGCGCTCCGCGCACCGCTGTGGTGTGGTGTGGTGTGGTGTGGTGT | 1020 |
| Qy | 1021 | CCCGCGCTGACGCTCCACGGGCAACGCTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG | 1080 |
| Ds | 1021 | CCCGCGCTGACGCTCCACGGGCAACGCTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG | 1080 |
| Qy | 1081 | AAGAGCGTGTGGGCGCTCAGTGGGCGCTGTGGATCCGAGCGGCTCTGGTGGATATC | 1140 |
| Ds | 1081 | AAGAGCGTGTGGGCGCTCAGTGGGCGCTGTGGATCCGAGCGGCTCTGGTGGATATC | 1140 |
| Qy | 1141 | AACGTTACCTCATCATCGGATCTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG | 1200 |
| Ds | 1141 | AACGTTACCTCATCATCGGATCTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG | 1200 |
| Qy | 1201 | TTGTACTCTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG | 1260 |
| Ds | 1201 | TTGTACTCTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG | 1260 |
| Qy | 1261 | CCACCGT | 1320 |
| Ds | 1261 | CCACCGT | 1320 |
| Qy | 1321 | AGGTTGT | 1380 |
| Ds | 1321 | AGGTTGT | 1380 |
| Qy | 1381 | CAGCTGTCTCGAAGATTTGTTAAATCCTCCCACTGAACACGACGACGACGACGACG | 1440 |
| Ds | 1381 | CAGCTGTCTCGAAGATTTGTTAAATCCTCCCACTGAACACGACGACGACGACGACG | 1440 |
| Qy | 1441 | TGGGTTACTCTGCTCCCTGAGAGCAAGGATGACAGCTGTGTGTGTGTGTGTGTGTGT | 1500 |
| Ds | 1441 | TGGGTTACTCTGCTCCCTGAGAGCAAGGATGACAGCTGTGTGTGTGTGTGTGTGTGT | 1500 |
| Qy | 1501 | GGCATTCTACGGGCTGGTCCAGAGAGGCTGATCAGAGTGGCCAACTATCCAGTGGCA | 1560 |
| Ds | 1501 | GGCATTCTACGGGCTGGTCCAGAGAGGCTGATCAGAGTGGCCAACTATCCAGTGGCA | 1560 |
| Qy | 1561 | ACACAGAACAGAGGAGAGAGAGTGTCCCTCCAGTGGGTTGGGTTGGGTTGGGTTGGG | 1620 |
| Ds | 1561 | ACACAGAACAGAGGAGAGAGAGTGTCCCTCCAGTGGGTTGGGTTGGGTTGGGTTGGG | 1620 |
| Qy | 1621 | AGCTGGAGCTTTAAATAGGACACAGGACACCGCAACATCCGTTCCGTTGGTGGG | 1680 |
| Ds | 1621 | AGCTGGAGCTTTAAATAGGACACAGGACACCGCAACATCCGTTCCGTTGGTGGG | 1680 |
| Qy | 1681 | GACAAATTCATTCCAGGATCTCTGCAATCATCTCCATCCGCGACGAGGCTACTAAC | 1740 |
| Ds | 1681 | GACAAATTCATTCCAGGATCTCTGCAATCATCTCCATCCGCGACGAGGCTACTAAC | 1740 |

Db 1681 GACAAATTCATTAATCCAGGATCTCTGCAATCATCTGCAATCCGCGAGAGCGCTACTATAC 1740
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Db 1741 AGCCAAATTTGACAAATGACTTCAATACTTCGCAAAAAGAGAGAGAGACCAAGAAAAG 1800
Qy 1801 AAGAAAAAGAAAGAGGTAACAGAGACCAAGAGAAAAGAGAAAGAGAGAGAGAGAGAGAG 1860
Db 1801 AAGAAAAAGAAAGAGGTAACAGAGACCAAGAGAAAAGAGAAAGAGAGAGAGAGAGAGAG 1860
Qy 1861 GACACAGTGACCAAGTGAAGTCTCAATGGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
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Qy 1921 AATGGCAATCTCTCCATGTAGCAATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1980
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Qy 1981 CTTAGAGACCTCAGAAATCTGCAAGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2040
Db 1981 CTTAGAGACCTCAGAAATCTGCAAGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2040
Qy 2041 GTTTTGTGTAAGAGCTTTACTAAGTCTGCTGTTAACTCTCTCTCTCTCTCTCTCTCTCTCT 2100
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Db 2101 TTTGAAACCTTAAAG 2160
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Qy 2221 TGACACTTGACAGGAG 2280
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Db 2521 AAGAGTCTGTTGGCTGTGAGTCAATATACCTAATCTGCAATCAATGCAAGAGAGAGAGAG 2580
Qy 2581 GTTCACTGTTTAAAG 2640
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Qy 2701 AGATCCCTTTTCCAAATCTATGCAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2760
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Qy 2761 GTTGTGTGTTCTATGAGATTTATTAATAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820
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Qy 2821 GAGAAATGATATACAAATCCCTAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2880
Db 2821 GAGAAATGATATACAAATCCCTAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2880
Qy 2881 TTAATGATCAATCTGCTACAGAGTCTTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2940
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Db 2941 TATCGGCCAGCTGCGCAATCACAGCTTTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3000
Qy 3001 ATGTATTACTTAATAAATGATCT 3060
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Qy 3061 TTATGTGACTTTGATACACACCT 3120
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Qy 3121 AAGAAATATGTTTCTCATACAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3180
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Qy 3181 TGTCTGTGTGTGCTAGCCTACACCT 3240
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Qy 3241 TGAATGTCAATCTTACTAACAACCTATGATGTTAAGTGAATCAATCTCTCTCTCTCTCTCTCT 3300
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Qy 3301 CTGTATGCTATGCTAAG 3360
Db 3301 CTGTATGCTATGCTAAG 3360
Qy 3361 AATGCAACTATTACCTAG 3420
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Qy 3421 TTCTTTTGTACAGCTGTGAG 3480
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Qy 3481 TTTGTGTATGAG 3520
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RESULT 5
AF152308
LOCUS AF152308 5233 bp mRNA linear PRI 22-JUL-1999

DEFINITION Homo sapiens protocadherin alpha 12 (PCDH-alpha12) mRNA, complete cds.

ACCESSION AF152308

VERSION AF152308.1 GI:5456901

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 5233)

AUTHORS Wu, Q. and Maniatis, T.

TITLE A striking organization of a large family of human neural cadherin-like cell adhesion genes

JOURNAL Cell 97 (6), 779-790 (1999)

MEDLINE 99386636

PUBMED 10380929

REFERENCE 2 (bases 1 to 5233)

AUTHORS Wu, Q. and Maniatis, T.

TITLE Human protocadherin genes

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 5233)

AUTHORS Wu, Q. and Maniatis, T.

TITLE Direct Submission

JOURNAL Submitted (17-MAY-1999) Department of Molecular and Cellular Biology, Harvard University, 7 Divinity Avenue, Cambridge, MA 02138, USA

FEATURES

source

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ORIGIN

Query Match 99.8%; Score 3513.6; DB 9; Length 5233;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 3516; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DB 949 GAATTCAGGTTAAGCCATTGATTAAGGGATTCCTTCATGCGAGGTCACAGCATGGTC 1008

QY 61 CTGGTGGAAATCTGGAGCGTGAATGCAATGTCCCTGAACTAATGTACTTACTTCTG 120

DB 1009 CTGGTGGAAATCTGGAGCGTGAATGCAATGTCCCTGAACTAATGTACTTACTTCTG 1068

QY 121 CTCCTCTGCAAGAGGATGCTCAGGTGGTACCGTCATTGCCCTGATTAGCGTGTGGAT 180

DB 1069 CTCCTCTGCAAGAGGATGCTCAGGTGGTACCGTCATTGCCCTGATTAGCGTGTGGAT 1128

QY 181 CGTGACTCTGGAAGCAATGACAGGTCAATCTGCTCACTGACACCTCATGTTCCCTCAAG 240

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QY 241 CTGGTGTCACTTACAGAAATTAATCTGTTGGTGTGGTGGTGGTGGTGGTGGTGGTGG 300

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QY 301 AGCGTGTGCGGCTATGAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360

DB 1249 AGCGTGTGCGGCTATGAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1308

QY 361 GCGAGCGTAGAGTGTCCGTGGAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 420

DB 1309 GCGAGCGTAGAGTGTCCGTGGAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1368

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QY 481 GTGTGGCATGGAGCGGACGCGACGCTGTGAGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 540

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DB 1489 CGCGGGTGGGCGAGCACGACCTGTGAGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 1548

QY 601 GTGTAGCGGTGACGCGGCTAGACACGAGGAGCTGGAGCTGTGAGTGTGAGTGTGAGTGTGAGC 660

DB 1549 GTGTAGCGGTGACGCGGCTAGACACGAGGAGCTGGAGCTGTGAGTGTGAGTGTGAGTGTGAGC 1608

QY 661 GCGCGGACGCGCGGCTGTGCGGCTCTGGGCGACGACGCTGACGCTGACGCTGTGCTGTGCTG 720

DB 1609 GCGCGGACGCGCGGCTGTGCGGCTCTGGGCGACGACGCTGACGCTGACGCTGTGCTGTGCTG 1668

QY 721 GACGAGAACGACCAACGCGCGGCTGTGCTGGGCGACGCTGCGGCTGGGCGACGCGGCGGCGCA 780

DB 1669 GACGAGAACGACCAACGCGCGGCTGTGCTGGGCGACGCTGCGGCTGGGCGACGCGGCGGCGCA 1728

QY 781 GTTAGGAGTGTGTAACCGGCTGTGGTGGTGGGCGGCGGCTGTGGTGGGCGGCGGCGGCGG 840

DB 1729 GTTAGGAGTGTGTAACCGGCTGTGGTGGTGGGCGGCGGCTGTGGTGGGCGGCGGCGGCGG 1788

QY 841 GTTAGGAGTGTGTAACCGGCTGTGGTGGTGGGCGGCGGCTGTGGTGGGCGGCGGCGGCGG 900

DB 1789 GTTAGGAGTGTGTAACCGGCTGTGGTGGTGGGCGGCGGCTGTGGTGGGCGGCGGCGGCGG 1848

[illegible]

Search completed: April 3, 2004, 11:14:40
Job time : 9064.41 secs

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | Query | | | | ID | Description |
|--------|--------|-------|-------|--------|----------|--------------------|
| | No. | Score | Match | Length | | |
| 1 | 3520 | 100.0 | 3520 | 4 | AAF29361 | Aaf29361 Amyloid-b |
| 2 | 3520 | 100.0 | 3520 | 9 | AAF93909 | Aaf93909 Human cDN |
| 3 | 3091.6 | 87.8 | 6338 | 9 | ADE31362 | Ade31362 Human dia |
| 4 | 2101.2 | 59.7 | 3748 | 5 | AAF98729 | Aaf98729 Human lat |
| 5 | 2101.2 | 59.7 | 3748 | 7 | AAF31944 | Aaf31944 Human bre |
| 6 | 1874.8 | 53.3 | 2826 | 5 | AS87420 | As87420 DNA encod |
| 7 | 1651.4 | 46.9 | 6230 | 5 | AA542520 | Aa542520 Human cDN |
| 8 | 1533 | 43.6 | 8035 | 5 | AA587421 | As87421 DNA encod |
| 9 | 1512 | 43.0 | 2850 | 5 | AA587419 | As87419 DNA encod |
| 10 | 1173.6 | 33.3 | 2827 | 7 | ACC00399 | Acc00399 Human cel |
| 11 | 1167.6 | 33.2 | 1356 | 4 | AA531272 | Aa531272 Human cDN |
| 12 | 1167.6 | 33.2 | 1356 | 6 | AQC66596 | Aqc66596 Human pol |
| 13 | 1167.6 | 33.2 | 1356 | 9 | ADC10618 | Adc10618 Human cDN |

14 1054.6 30.0 2574 7 ACC00400
 15 1352 29.9 3045 7 ACC00401
 c 16 1051.2 29.9 7893 5 AAF76447
 c 17 857.8 24.4 2360 5 AAS65427
 c 18 738.2 21.0 1047 6 ABQ16376
 c 19 738.2 21.0 1047 6 ABQ16377
 c 20 677.6 19.2 1228 6 ABQ16381
 c 21 677.6 19.2 1228 6 ABQ16380
 c 22 676.8 19.2 2884 5 ADB62335
 c 23 638 18.1 1047 6 ABQ16374
 c 24 638 18.1 1047 6 ABQ16375
 c 25 627.2 17.8 1057 6 ABQ16373
 c 26 627.2 17.8 1057 6 ABQ16372
 c 27 623.2 17.7 750 5 AAF94096
 c 28 622.8 17.7 1139 6 ABQ16400
 c 29 622.8 17.7 1139 6 ABQ16401
 c 30 606.8 17.2 1151 6 ABQ16404
 c 31 606.8 17.2 1151 6 ABQ16405
 c 32 601.2 17.1 1166 6 ABQ16421
 c 33 601.2 17.1 1166 6 ABQ16420
 c 34 594.4 16.9 1084 6 ABQ16392
 c 35 594.4 16.9 1084 6 ABQ16393
 c 36 584.8 16.6 1060 6 ABQ16389
 c 37 584.8 16.6 1060 6 ABQ16388
 c 38 565 16.1 1015 6 ABQ16412
 c 39 565 16.1 1015 6 ABQ16413
 c 40 559.2 15.9 974 6 ABQ16424
 c 41 559.2 15.9 974 6 ABQ16425
 c 42 553 15.7 1228 6 ABQ16379
 c 43 553 15.7 1228 6 ABQ16378
 c 44 534.2 15.2 950 6 ABQ16396
 c 45 534.2 15.2 950 6 ABQ16397

ALIGNMENTS

RESULT 1
 ID AAF29361 standard; DNA: 3520 BP.
 XX AC AAF29361;
 XX DT 20-APR-2001 (first entry)
 XX DE Amyloid-beta protein agglutination regulating factor DNA SEQ ID 9.
 XX KW Human; amyloid-beta protein agglutination regulating factor;
 XX KW Alzheimer's disease; ds.
 XX OS Homo sapiens.
 XX EN WO200104299-A1.
 XX PD 18-JAN-2001.
 XX PF 06-JUL-2000; 2000WO-JP004515.
 XX PR 08-JUL-1999; 95JP-00194179.
 XX PR 18-OCT-1999; 95JS-0159586P.
 XX PA (HELI-) HELIX RES INST.

PI Ota T, Isegai T, Nishikawa T, Kawai Y, Yamazaki M, Satoh S;
 FI Arakawa H, Morita M;
 XX WFI; 2001-138347/14.
 DR P-P5DB; A3549771.
 XX Polynucleotide encoding Amyloid-beta protein agglutination-controlling
 PT factor, useful for inhibiting or promoting agglutination or sedimentation
 PT of amyloid-beta protein and in diagnosis and screening drugs for
 PT Alzheimer's disease.
 XX Claim 1; Page 58-63; 72pp; Japanese.
 CC This invention relates to polynucleotides AAF29357 - AAF29361 which
 CC encode proteins AAF49767 - AAF49771. The proteins inhibit or promote the
 CC agglutination of amyloid beta protein. The protein and polynucleotide
 CC sequences are useful in the diagnosis of Alzheimer's disease. They are
 CC also useful for screening drugs which are useful for treating Alzheimer's
 CC disease
 XX Sequence 3520 BP; 871 A; 896 C; 901 G; 852 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 3520; DB 4; Length 3520;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3520; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAATTCAGGTTAAGCCATGATGAAGGATTCCTTCATGGCAGGTGACAGCATGGTC 60
 DB 1 GAATTCAGGTTAAGCCATGATGAAGGATTCCTTCATGGCAGGTGACAGCATGGTC 60
 QY 61 CTGGTGGAAATCTGAGCGTGAATGACATGCTCCCTGAAGTAATGTTACTTCACTGTG 120
 DB 61 CTGGTGGAAATCTGAGCGTGAATGACATGCTCCCTGAAGTAATGTTACTTCACTGTG 120
 QY 121 CTCCCTGTGCAAGAGGATGCTCAGGTGGGTACCGTCAATGCCCTGATTAGCGGTGCGGAT 180
 DB 121 CTCCCTGTGCAAGAGGATGCTCAGGTGGGTACCGTCAATGCCCTGATTAGCGGTGCGGAT 180
 QY 181 CGTGACTCTGGACCCATGGACAGGTCATCTGCTCACTGACACCTCATGTTCCCTTCAG 240
 DB 181 CGTGACTCTGGACCCATGGACAGGTCATCTGCTCACTGACACCTCATGTTCCCTTCAG 240
 QY 241 CTGGTGTCCACCTACAGATTACTACTGTTGGTGTGCTGACAGCGCCCTGACCGCGAG 300
 DB 241 CTGGTGTCCACCTACAGATTACTACTGTTGGTGTGCTGACAGCGCCCTGACCGCGAG 300
 QY 301 AGCGTGTGGCGCTATGAGCTGTTGTTGCTGCTGCGGGGATGGGGGCTGCTTGGCTGG 360
 DB 301 AGCGTGTGGCGCTATGAGCTGTTGTTGCTGCTGCGGGGATGGGGGCTGCTTGGCTGG 360
 QY 361 GCCAGGCTAGAGTGTCCGTGGAGTGGCGGATGGGGGCTGCGCTTGGCTGG 420
 DB 361 GCCAGGCTAGAGTGTCCGTGGAGTGGCGGATGGGGGCTGCGCTTGGCTGG 420
 QY 421 CAGCCCGAGTACACAGTGTCTGTGAAGGAGAAACACCGCGGCTGCCACATCTTCAG 480
 DB 421 CAGCCCGAGTACACAGTGTCTGTGAAGGAGAAACACCGCGGCTGCCACATCTTCAG 480
 QY 481 GTGTGGGATGGGACCGGACGCGCAGAAAGAACGCGCTGTCTACTCGCTGGTGGAG 540
 DB 481 GTGTGGGATGGGACCGGACGCGCAGAAAGAACGCGCTGTCTACTCGCTGGTGGAG 540
 QY 541 CCGCGGGTGGGCGAGCAGCAGCTGTCTGAGCTAGTGTGCTGCTGACGCGGAGAGCGGAG 600

| | | | |
|----|------|--|------|
| Qy | 1501 | GGCATTCTACGGGCTGGTCCAGAGGAGGCGCTGATCTAGCAGTGGTGGCCAACTAGTATCCAGTGC | 1560 |
| Dd | 1501 | GGCATTCTACGGGCTGGTCCAGAGGAGGCGCTGATCAGCAGTGGCCAACTAGTATCCAGTGC | 1560 |
| Qy | 1561 | ACAACAGAAACCAAGCAGAGGAGAAAGTGTCCCTCCAGCTCGCTGGTGGGAGTGTCAACAACAAC | 1620 |
| Dd | 1561 | ACAACAGAAACCAAGCAGAGGAGAAAGTGTCCCTCCAGCTCGCTGGTGGGAGTGTCAACAACAAC | 1620 |
| Qy | 1621 | AGCTGGACCTTTAAATAGGACCAAGGCAACCCCAAAACAAATCCGGTCCCGGAGTGGTGC | 1680 |
| Dd | 1621 | AGCTGGACCTTTAAATAGGACCAAGGCAACCCCAAAACAAATCCGGTCCCGGAGTGGTGC | 1680 |
| Qy | 1681 | GACAAATTCATTCCAGGATCTCTCTGCAATCATCTCTCCATCTCGGCAAGAGCTCTCAAC | 1740 |
| Dd | 1681 | GACAAATTCATTCCAGGATCTCTCTGCAATCATCTCTCCATCTCGGCAAGAGCTCTCAAC | 1740 |
| Qy | 1741 | AGCCAAATTCACAAAGTACTTCATAACCTTGGCAAAAGGAGGAGACCAAGAAAG | 1800 |
| Dd | 1741 | AGCCAAATTCACAAAGTACTTCATAACCTTGGCAAAAGGAGGAGACCAAGAAAG | 1800 |
| Qy | 1801 | AAAGAAAAGAGAGGTTAACAAGACCCAGAGCAAAAAGAAAGGAGGAGCAACAGCAGCT | 1860 |
| Dd | 1801 | AAAGAAAAGAGAGGTTAACAAGACCCAGAGCAAAAAGAAAGGAGGAGCAACAGCAGCT | 1860 |
| Qy | 1861 | GACACAGTGAACCGTAGGTCTCTCAATGGAAACAAGCAGCTTAGCAGCTTTTGTAAT | 1920 |
| Dd | 1861 | GACACAGTGAACCGTAGGTCTCTCAATGGAAACAAGCAGCTTAGCAGCTTTTGTAAT | 1920 |
| Qy | 1921 | AATGGCAATCTCTCCATGTAGCAATTCCTGCTCTTTCTCTATCTACACAGGCGCT | 1980 |
| Dd | 1921 | AATGGCAATCTCTCCATGTAGCAATTCCTGCTCTTTCTCTATCTACACAGGCGCT | 1980 |
| Qy | 1981 | CTTAGAGACCTCAGAAATCTGCAGAAAGTTCCTGTGTCTGTCTAGAACGCATTTAACG | 2040 |
| Dd | 1981 | CTTAGAGACCTCAGAAATCTGCAGAAAGTTCCTGTGTCTGTCTAGAACGCATTTAACG | 2040 |
| Qy | 2041 | GTTTTGTGTAAAGCTTTACTAAGTCTGGTGTAACTCTTTCTCTCTCCACTCTGGTGT | 2100 |
| Dd | 2041 | GTTTTGTGTAAAGCTTTACTAAGTCTGGTGTAACTCTTTCTCTCCACTCTGGTGT | 2100 |
| Qy | 2101 | TTTCAGACCTTAAAGACAGACCGAGTTTCCTTTCTCTCCGCGCAAGGAGAGGCTT | 2160 |
| Dd | 2101 | TTTCAGACCTTAAAGACAGACCGAGTTTCCTTTCTCTCCGCGCAAGGAGAGGCTT | 2160 |
| Qy | 2161 | CCAGCCCGCGCAAGTGAAGGTTGGACTCTCTGCGCTGTGCTCGGGAGATCCTGTCTGA | 2220 |
| Dd | 2161 | CCAGCCCGCGCAAGTGAAGGTTGGACTCTCTGCGCTGTGCTCGGGAGATCCTGTCTGA | 2220 |
| Qy | 2221 | TGACATCTGAGGCGCAGGCTGAAGAATTTGAGATTAGACAGCTTCGGAGTTTGGGCA | 2280 |
| Dd | 2221 | TGACATCTGAGGCGCAGGCTGAAGAATTTGAGATTAGACAGCTTCGGAGTTTGGGCA | 2280 |
| Qy | 2281 | CTGGGTGTGTAGCTACCGCGGTATGCAGTGGCCAGATATGGCTGAGACAGGACGAC | 2340 |
| Dd | 2281 | CTGGGTATGTGTAGCTACCGCGGTATGCAGTGGCCAGATATGGCTGAGACAGGACGAC | 2340 |
| Qy | 2341 | TTAGACTAATTTGGTACAGGAGGCAAGAAACAAGAGCAATAATAACGCGGAAGTTATC | 2400 |
| Dd | 2341 | TTAGACTAATTTGGTACAGGAGGCAAGAAACAAGAGCAATAATAACGCGGAAGTTATC | 2400 |
| Qy | 2401 | AGTATGGAGGGAAGTGTAACTTTAAAGGACACAGCTTTCTAAATCTTCAACTCAAGA | 2460 |
| Dd | 2401 | AGTATGGAGGGAAGTGTAACTTTAAAGGACACAGCTTTCTAAATCTTCAACTCAAGA | 2460 |

| | | | | | |
|-----------|---|---|------|--|--|
| Db | 3361 | AAAGCACTATPACTAGAGTGAACCTTTTACGCTTTATTTGTTGAAGTAAATTCACATATAT | 3420 | | |
| Qy | 3421 | TTCCCTTTGTACACCTGTGAAAAAGTGAGGTAGTGTCTTTTAAACCAATGTAAACAGCT | 3480 | | |
| Db | 3421 | TTCCCTTTGTACACCTGTGAAAAAGTGAGGTAGTGTCTTTTAAACCAATGTAAACAGCT | 3480 | | |
| Qy | 3481 | TTTGTGATGAAGACACAGATAAAATTTCTTTCTTAATC | 3520 | | |
| Db | 3481 | TTTGTGATGAAGACACAGATAAAATTTCTTTCTTAATC | 3520 | | |
| RESULT 2 | | | | | |
| AAAF93909 | standard; cDNA; 3520 BP. | | | | |
| XX | AAAF93909; | | | | |
| XX | 23-MAY-2001 (first entry) | | | | |
| XX | Human cDNA encoding a membrane or secretory protein clone PSEC0256. | | | | |
| DE | Human; secretory protein; membrane protein; vaccine; gene therapy; | | | | |
| KW | rheumatoid arthritis; diabetes; ss. | | | | |
| KW | Homo sapiens. | | | | |
| XX | EF1967182-A2. | | | | |
| XX | 10-JAN-2001. | | | | |
| PD | 07-JUL-2000; 2000EP-0C114090. | | | | |
| XX | 08-JUL-1999; 99JP-00194179. | | | | |
| PP | 11-JAN-2000; 2000JP-00118775. | | | | |
| XX | 02-MAY-2000; 2000JP-00183766. | | | | |
| XX | (HELI-) HELIX RES INST. | | | | |
| XX | Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K; | | | | |
| PI | WPI; 2001-093969/11. | | | | |
| XX | P-FSDS; AAB88462. | | | | |
| DR | Nucleic acids encoding secretory proteins/membrane proteins, useful in | | | | |
| DR | gene therapy or as candidate target molecules in drug development. | | | | |
| XX | Claim 1; SEQ ID NO 331; 609pp + Sequence Listing; English. | | | | |
| XX | This invention relates to nucleic acid sequences AAF93744 - AAF93916 | | | | |
| XX | which encode human secretory or membrane proteins represented by AAB88317 | | | | |
| XX | - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and | | | | |
| CC | AAAF6232 - AAF62235 which are used to isolate the cDNA sequences of the | | | | |
| CC | invention. The invention also includes methods for the production of | | | | |
| CC | antibodies directed against the proteins, and cDNA sequences, which can | | | | |
| CC | be used in vaccines. The polynucleotide sequences can be used in gene | | | | |
| CC | therapy. The polynucleotide sequences and the proteins they encode may be | | | | |
| CC | used in the prevention, treatment and diagnosis of diseases associated | | | | |
| CC | with inappropriate secretory protein/membrane protein expression. The | | | | |
| CC | nucleic acids and complementary sequences may also be used as DNA probes | | | | |
| CC | in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect | | | | |
| CC | and quantitate the presence of similar nucleic acid sequences in samples. | | | | |
| CC | They may also be used to study the expression and function of secretory | | | | |
| CC | proteins/membrane polypeptides and their role in metabolism. | | | | |

1661 GACAAATTCATTATCCAGAGATCTCCTGCAATCATCTCCATCCGGCAGAGGCTACTAAC 1740
1661 GACAAATTCATTATCCAGAGATCTCCTGCAATCATCTCCATCCGGCAGAGGCTACTAAC 1740
1741 AGCCAAATTCAGAAAAGTGAATCTATTAACCTTCGGCAAAAGAGAGAGAGAGAGAGAG 1800
1741 AGCCAAATTCAGAAAAGTGAATCTATTAACCTTCGGCAAAAGAGAGAGAGAGAGAGAG 1800
1801 AAGAAAAG 1860
1801 AAGAAAAG 1860
1861 GACAAAG 1920
1861 GACAAAG 1920
1921 AATGGCAAAATCTCTCCCATGTAGCAATTCCTGCTGCTCTCTCTCTCTCTCTCTCTCT 1980
1921 AATGGCAAAATCTCTCCCATGTAGCAATTCCTGCTGCTCTCTCTCTCTCTCTCTCTCT 1980
1981 CTTAG 2040
1981 CTTAG 2040
2041 GTTTTGTCTGTAAGAGCTTTACTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
2041 GTTTTGTCTGTAAGAGCTTTACTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
2101 TTTGAG 2160
2101 TTTGAG 2160
2161 CCGAG 2220
2161 CCGAG 2220
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2341 TTAGACTAATTTGTTACAG 2400
2341 TTAGACTAATTTGTTACAG 2400
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2401 AGTATGGAGGAG 2460
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2521 AAGGTCTGTTGGCTGTAG 2580
2581 GTTCAGTGTTTTAAAG 2640

2581 GTTCAGTGTTTTAAAG 2640
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2701 AGATCCTTTTCCCAATCTACTTATGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAG 2760
2701 AGATCCTTTTCCCAATCTACTTATGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAG 2760
2761 GTTGTGTCTTCATAGATTATTTAAATAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820
2761 GTTGTGTCTTCATAGATTATTTAAATAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820
2821 GAGAAATGAATAACAAATTCCT 2880
2821 GAGAAATGAATAACAAATTCCT 2880
2881 TTAATGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940
2881 TTAATGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940
2941 TATGCGGCACTGCGCAATCAGAGCTTTACTCTTTTCAAGTCACTCTGCGGCTGCTCTGCTGCT 3000
2941 TATGCGGCACTGCGCAATCAGAGCTTTACTCTTTTCAAGTCACTCTGCGGCTGCTCTGCTGCT 3000
3001 AAGTATTAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3060
3001 AAGTATTAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3060
3061 TATGCTGCACTTTGATACAG 3120
3061 TATGCTGCACTTTGATACAG 3120
3121 AAGAAATAATTTGTTTCTCATACAGTGAAGGAGATTTTCAATCTACTTAATCTCTGACT 3180
3121 AAGAAATAATTTGTTTCTCATACAGTGAAGGAGATTTTCAATCTACTTAATCTCTGACT 3180
3181 TGTCTGTGTGCTAGAGCTGACAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3240
3181 TGTCTGTGTGCTAGAGCTGACAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3240
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3361 AATGCAACTATTAACCTAG 3420
3361 AATGCAACTATTAACCTAG 3420
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3421 TTTCTTTTGTACAGCTGTGAAAG 3480
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2004, 11:14:53 ; Search time 845.87 Seconds
(without alignments)
15564.412 Million cell updates/sec

Title: US-10-030-269A-9
Perfect score: 3520
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Scoring table: IDENTITY NJC
Gapop 10.0 , Gapext 1.0

Searched: 2466186 seqs, 1870095123 residues

Total number of hits satisfying chosen parameters: 4932372

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No. | Score | Query Match | Length | DB ID | Description |
|--------|--------|-------|-------------|--------|---------------------|-------------------|
| 1 | 2101.2 | 59.7 | 3748 | 14 | US-10-176-847-101 | Sequence 101, App |
| 2 | 1167.6 | 33.2 | 1356 | 9 | US-09-764-870-86 | Sequence 86, Appl |
| 3 | 1167.6 | 33.2 | 1356 | 14 | US-10-125-540-86 | Sequence 86, Appl |
| 4 | 1103.4 | 31.3 | 1105 | 14 | US-10-029-386-22917 | Sequence 22917, A |
| 5 | 769.4 | 21.9 | 1037 | 14 | US-10-029-386-22808 | Sequence 22808, A |

6 677.2 19.2 834 14 US-10-029-386-22888
c 7 676.8 19.2 2884 15 US-10-04-047-489
c 8 651.8 18.5 849 14 US-10-029-386-25221
c 9 570 16.2 570 14 US-10-029-386-3758
c 10 556 15.8 556 14 US-10-029-386-24103
c 11 551.4 15.7 553 14 US-10-029-386-9214
c 12 548 15.6 548 14 US-10-029-386-13109
c 13 538 15.3 720 14 US-10-029-386-20243
c 14 532 15.1 2894 15 US-10-161-493-119
c 15 512.4 14.6 514 14 US-10-029-386-10398
c 16 506 14.4 708 14 US-10-029-386-24195
c 17 505.8 14.4 591 14 US-10-029-386-2214
c 18 503.2 14.3 588 14 US-10-029-386-4336
c 19 501.6 14.3 577 14 US-10-029-386-11514
c 20 492 14.0 580 14 US-10-029-386-2131
c 21 489.6 13.9 547 9 US-09-864-761-7683
c 22 478.2 13.6 563 14 US-10-029-386-2659
c 23 473.2 13.4 550 14 US-10-029-386-2749
c 24 465.4 13.2 467 9 US-09-864-761-24387
c 25 462 13.1 574 14 US-10-029-386-2082
c 26 460 13.1 524 14 US-10-029-386-11711
c 27 449.2 12.8 518 14 US-10-029-386-6513
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c 29 444 12.6 557 14 US-10-029-386-10344
c 30 438.2 12.4 523 14 US-10-029-386-25028
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c 32 436 12.4 580 14 US-10-029-386-3754
c 33 434.8 12.4 559 14 US-10-029-386-24053
c 34 432.4 12.3 630 14 US-10-029-386-25414
c 35 422.2 12.0 571 14 US-10-029-386-9096
c 36 422 12.0 451 10 US-09-918-995-10991
c 37 415 11.8 415 14 US-10-029-386-17458
c 38 414.8 11.8 522 14 US-10-029-386-11315
c 39 413.8 11.8 420 10 US-09-960-706-107
c 40 411 11.7 452 10 US-09-918-995-13437
c 41 402.8 11.4 462 14 US-10-029-386-15914
c 42 391 11.1 533 9 US-09-864-761-12100
c 43 391 11.1 533 14 US-10-029-386-16264
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c 45 373 10.6 413 14 US-10-029-386-18036

Search completed: April 4, 2004, 00:36:51
Job time : 851.87 secs

Sequence 22888, A
Sequence 489, App
Sequence 25221, A
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Sequence 9214, Ap
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Sequence 24195, A
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Sequence 2749, Ap
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Sequence 11315, A
Sequence 107, App
Sequence 13437, A
Sequence 15914, A
Sequence 12100, A
Sequence 16264, A
Sequence 3260, Ap
Sequence 18036, A

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2004, 01:46:51 ; Search time 5955.22 Seconds
(without alignments)
17650.980 Million cell updates/sec

Title: US-10-030-269A-9

Perfect score: 3520

Sequence: 1 gaattacaggttaacgcaat.....taaaattttttttaaatc 3520

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_est4:*
13: gb_est5:*
14: gb_estfun:*
15: em_estfun:*
16: em_eston:*
17: em_gas_hum:*
18: em_gas_inv:*
19: em_gas_pln:*
20: em_gas_vrt:*
21: em_gas_fun:*
22: em_gas_mam:*
23: em_gas_mus:*
24: em_gas_pro:*
25: em_gas_fod:*
26: em_gas_phg:*
27: em_gas_vrt:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|--------|-------------|--------|----|----------|--------------------|
| 1 | 1356.2 | 38.5 | 2754 | 11 | AK043822 | AK043822 Mus muscu |
| 2 | 1185.2 | 33.7 | 2891 | 11 | BC030857 | BC030857 Mus muscu |
| 3 | 1177.2 | 33.4 | 2878 | 11 | AK043705 | AK043705 Mus muscu |
| 4 | 875.2 | 24.9 | 2894 | 11 | AK048980 | AK048980 Mus muscu |
| 5 | 864.2 | 24.6 | 917 | 13 | BQ424699 | BQ424699 AGENCOURT |
| 6 | 746.6 | 21.2 | 839 | 12 | BI831598 | BI831598 603074629 |
| 7 | 745.4 | 21.2 | 773 | 12 | BI753524 | BI753524 603026670 |
| 8 | 736.4 | 20.9 | 739 | 14 | CD239823 | CD239823 FNPBVH12 |
| 9 | 716.4 | 20.4 | 912 | 9 | AA626775 | AA626775 ad09e07.s |
| 10 | 708.4 | 20.0 | 763 | 10 | BF983147 | BF983147 602305866 |
| 11 | 698.4 | 19.8 | 720 | 14 | CA436984 | CA436984 UI-H-DF1- |
| 12 | 697.4 | 19.8 | 703 | 12 | BM685644 | BM685644 UI-E-CIO- |
| 13 | 637.6 | 18.1 | 847 | 10 | BF793430 | BF793430 602254901 |
| 14 | 626.4 | 17.8 | 678 | 12 | BI850525 | BI850525 imagegc.1 |
| 15 | 591.8 | 16.8 | 957 | 13 | BQ720698 | BQ720698 AGENCOURT |
| 16 | 575.4 | 16.3 | 584 | 13 | BU071903 | BU071903 im35908.y |
| 17 | 566.4 | 16.1 | 575 | 13 | BU071607 | BU071607 im43510.y |
| 18 | 551.4 | 15.7 | 554 | 9 | AI268404 | AI268404 qm05e10.x |
| 19 | 545.2 | 15.5 | 749 | 12 | BG709151 | BG709151 602675025 |
| 20 | 536.6 | 15.2 | 787 | 13 | BU750609 | BU750609 CH3#034.E |
| 21 | 528.8 | 15.0 | 736 | 12 | BI602140 | BI602140 603246261 |
| 22 | 528.6 | 15.0 | 562 | 28 | AQ483592 | AQ483592 RPCI-11-2 |
| 23 | 528.4 | 15.0 | 530 | 14 | CB218096 | CB218096 NISC.nb06 |
| 24 | 527.4 | 15.0 | 531 | 10 | BE043069 | BE043069 ho32e02.x |
| 25 | 526.8 | 15.0 | 587 | 12 | BG732993 | BG732993 346670.MA |
| 26 | 508.6 | 14.4 | 591 | 14 | CA396936 | CA396936 cs83r10.y |
| 27 | 506.4 | 14.4 | 828 | 14 | CF537889 | CF537889 UI-M-GIO- |
| 28 | 501.8 | 14.3 | 711 | 12 | BI599585 | BI599585 603247760 |
| 29 | 499.4 | 14.2 | 636 | 10 | BB641641 | BB641641 BB641641 |
| 30 | 498.8 | 14.2 | 502 | 9 | AI672463 | AI672463 wa03e05.x |
| 31 | 498 | 14.1 | 732 | 14 | CB518847 | CB518847 UI-M-GH3- |
| 32 | 495.8 | 14.1 | 502 | 9 | AA846453 | AA846453 aj56b03.s |
| 33 | 492.6 | 14.0 | 726 | 13 | BQ191879 | BQ191879 UI-R-DRI- |
| 34 | 483 | 13.7 | 569 | 14 | CB218095 | CB218095 NISC.nb06 |
| 36 | 475.2 | 13.5 | 853 | 14 | CD806992 | CD806992 UI-M-GWO- |
| 37 | 474.2 | 13.5 | 665 | 28 | BZ203894 | BZ203894 CH230-436 |
| 38 | 472.8 | 13.4 | 501 | 13 | BQ639025 | BQ639025 hd30e03.y |
| 39 | 462.4 | 13.1 | 970 | 13 | BQ947259 | BQ947259 AGENCOURT |
| 40 | 457 | 13.0 | 681 | 13 | BU280745 | BU280745 603863621 |
| 41 | 453.4 | 12.9 | 843 | 13 | RU249664 | RU249664 603321109 |
| 42 | 452.4 | 12.9 | 455 | 9 | AA973493 | AA973493 oa45e05.s |
| 43 | 452.4 | 12.9 | 455 | 10 | AW162420 | AW162420 au74e02.x |
| 44 | 447.6 | 12.7 | 679 | 14 | CF533624 | CF533624 UI-M-GH0- |
| 45 | 446.8 | 12.7 | 1019 | 12 | BI465306 | BI465306 603206625 |

Search completed: April 3, 2004, 16:37:45
Job time : 5963.42 secs